

## FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCCACGCGTCCGGGCCGGAGCAGCACGCGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCG  
CAGCGTACCCGCCATGCGCCTGCCGCGCCGGGCGCGCTGGGGCTCCTGCCGTTCTGCTG  
CTGCTGCCGCCCGCGCCGAGGCGCCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGCT  
GGTGGACAAGTTTAAACAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGCGGGAACA  
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATC  
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA  
GCACCTGGAGGCCCTGGTGGCTGCAGCTGAAGAGCGAATATCTGACTTATTTCGAGTGGTTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGC  
CAGGGCGGATCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA  
GGGCGACGGGTCTTGCCGTTGCCACATGGGGTACCAGGGCCCCGTGTGCACTGACTGCATGG  
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGTACGAGTCC  
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT  
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG  
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTG  
GGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA  
CGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAAAACCTGTGTGAGGAAAAACG  
AAAAGTGTCTACAATACCTCCAGGGAGCTACGTCTGTGTGTCTCTGACGGCTTCGAAGAAACG  
GAAGATGCCTGTGTGCCCGCCGCGAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT  
GCCCTCCCGCAAGACCTGTAAATGTGCCGGACTTACCCTTTAAATTATTCAGAAGGATGTCC  
CGTGGAATAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGCGGGGAGAGGCTGC  
CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTA  
AACAGACTTGTATATTTTGATACAGTTCCTTTGTAATAAAATTGACCATTTGTAGTAATCAGG  
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGCCGCACTCTAGAGTCGACCTGCAGAAGC  
TTGGCCGCCATGGCCCAACTTGTTTATTGCACTTATAATGGTTACAAATAAAGCAATAGCA  
TCACAAATTTACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCAAACTC  
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTGCGCGCAGCACCATGGCCTGAAAT  
AACCTCTGAAAGAGGAACCTTGGTTAGGTACCTTCTGAGGCGGAAAGAACAGCTGTGGAATG  
TGTGTCACTTAGGGTGTGGAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC  
ATCTCAATTAGTCAGCAACCCAGTTTT

CCGCGCGGAGGCTGCT

## FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop  
><MW: 38192, pI: 4.53, NX(S/T): 2  
MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEKTLISKYESSSEIRL  
LEILEGLCESSDFECNQMLEAQEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYPDCLACQGGGSRPCSG  
NGHCSGDSRGQDGSRCRCHMGYQGPLCTDCMDGYFSSLRNETHSICTACDESKCTCSGLTNRDGCEVGVWLDE  
GACVDVDECAAEPPPCSAQAQFCKNANGSYTCEECDSSCVGTGEGPGNCKECISGYAREHGQCADVDECSLAEKT  
CVRKNENCYNTPGSYVVCPCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL

### **Signal peptide:**

amino acids 1-24

### **N-glycosylation sites.**

amino acids 190-194 and 251-255

### **Glycosaminoglycan attachment sites.**

amino acids 149-153 and 155-159

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 26-30

### **Casein kinase II phosphorylation sites.**

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343  
and 349-353

### **Tyrosine kinase phosphorylation site.**

amino acids 303-310

### **N-myristoylation sites.**

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and  
313-319

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 308-320

### **EGF-like domain cysteine pattern signature.**

amino acids 166-178

### **Leucine zipper pattern.**

amino acids 94-116

[illegible]

AAGGTCACCAATGCACTCTGGTTCTATCGATTGAATTCCTCCCGGGGATCCTCTAGAGATCCCTC  
 GACCTCGACCCACGCGCTCCGCGAGGCCGGGAGGCGACGCCACGGCTCTAAACGGGAACA  
 GCGCTGGCTGAGGAGCTCGACGCGACGAGATATCTGACGGCCGAGTTCGTTAGTGGCG  
 GCACGAGGAGTTTTCGCGCAGCGAGGAGGTTCTGAGCAGCATGCCCGGAGGAGCGCCTTC  
 CCTGCGCGCGCTCTGGCTCTGGAGCATCTCTGTGCTGCTGGCATCTGCGGCTCGGAGGCG  
 CGGGCGCGCGCAGGAGGAGCACTGTACTTATGGAATCGATGCTTACACAGGCAAGAGTACTCA  
 TAGGATTTGAAGAAGATATCCTGATTGTTCAGAGGGGAAAATGGCACCCTTTTACACATGAT  
 TCTCAGAAAAGCGCAACAGAGAATGCCAGTATTCTCTGTCATATCCATTCCATGAATTTTAC  
 CTGGCAAGCTGCAAGGCGAGGCAATACTTCTATGAATTCCTGTCTTGCCTCGCTCCGTGATA  
 AAGGCATCATGCGAGATCAACCCGTCAATGTCTCTGTCTGCGGAACAGTGCCTCAACAGGCA  
 TCAGTTGTTCAAGTTGGTTTCCATGTCTTGGAAAAAGATGGGTTGGCAGCATTTTGAAT  
 GGATGTGATTGTTATGAATTCGAAGGCAACAACTTCTCCAAACACCTCAAAATGCTATCT  
 TCTTTAAACATGTGCAACAGCTGAGTGCCGAGGCGGAGTGCAGAAATGGAGGCTTTTGAAT  
 GAAAGACGATCTGCGAGTGCTCTGATGGGTTCCGCGGACTCACTGTGAGAAAGCCCTTTG  
 TACCCCATCATGATGTAATGGTGGACTTTGTGTGACTCTGTGTTTCTGCATCTGCCCCACCTG  
 GATTTCTAGGAGTGAATGTGACAAAGCAAACTGCTCAACACCTGCTTTAATGGAGGACCT  
 GTTTTCTACCTCGAAAATGTATTGCTCTCCAGAGTACAGGGAGAGCAGTGTGAATCAG  
 CAAATGGCCCAACCCCTGTGCAAAATGGAGGTAAATGCAATTGGTAAAGCAAAATGTAAGTGT  
 CCAAAGGTTACCAAGGAGACCTCTGTTCAAAGCTGTCTCGGAGCTGGCTGTGGTGACAT  
 GGAACCTGCCATGAAGCCCAACAAATGCGCAATCTCAAGAAAGTTGGCATGGAAGCACTGCGAA  
 TAAAGAGTCAAGAGCCAGCCTCATACATGCGCTGAGGCCACAGGCGCCAGCTCAGGCAGC  
 ACACGCCTTCACTTAAAGAGGCCGAGGAGCGGGGATCCACTGAATCAATTACATCTG  
TGAACTCCGACATCTGAAACGTTTTAAGTTACCCCAAGTTCATAGCCTTTGTTAACCTTTCA  
 TGTGTTGAATGTTCAAAATATGTTTCATTACTTCACTTAAAGATATCGCTGCAATTTATTAGCT  
 TCAATATAAATCTCAGTGTGATATTACTCTTCTTTTAAGTTTCTAAGTACGTCTGTAG  
 CATGATGGTATAGATTTTCTGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGA  
 TCAAGTTAAATTTTCAGTGTGATGTGGCAGATATTTTCAAAATTAACAATGCATTTATTGGT  
 GTCTGGGGCGAGGGGAATCAGAAAGGTTAAATTTGGGCAAAATGCGTAGTCACAAGAA  
 TGTGATGTGTGCAGTTAATGTTGAAGTTACAGCAATTTCAGATTTTATGTCAGATATTAGAT  
 TTGATTCACATTTTAAAAATGCTCTTAATTTTAAACTCTCAATACAATATATTTTGACC  
 TTACCAATTTTCCAGAGATTCAGTATAAAAAAAGGAAATTAACCTGTGGTAGTGGCAATTT  
 AAACAATATAATATTTCAAACCAATGAATTAAGGAATATAATGTATGAACCTTTTTCAT  
 TGGCTTGAAGCAATATAATATATTGTAACCAAAACACAGCTCTTACCTAATAAACAATTTTAT  
 ACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTTGGAAAAAAGGAAAAA  
 AAAAAAAGGAAAAAAGGCGGCGGCGCACTTAGAGTCGACCTCGCAAGCTTGGC  
 CGCCATGGCCCAACTGTTTATTTCAGCTTAAATG

## FIGURE 4

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFFAAALWLSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSE GK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGHPCHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSKPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW
```

### **Signal peptide:**

amino acids 1-28

### **N-glycosylation site.**

amino acids 88-92, 245-249

### **Casein kinase II phosphorylation site.**

amino acids 319-323

### **Tyrosine kinase phosphorylation site.**

amino acids 370-378

### **N-myristoylation sites.**

amino acids 184-190, 185-191, 189-195, 315-321

### **ATP/GTP-binding site motif A (P-loop).**

amino acids 285-293

### **EGF-like domain cysteine pattern signature.**

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTGCGAGAGCCAGGAGGCGGAGGCGCGGGGCCAGCCTGGG  
CCCCAGCCACACCTTCACCAGGGCCAGGAGGCCACCATGTGGCGATGTCCACTGGGGCTAC  
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCGTGGGCGCCGG  
GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCGGTACTGCCAGGA  
GCAGGACCTGTGCTGCCGCGGCGGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT  
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC  
TGCTCGGGCTGCCACCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA  
TCCAGTCTTGGGAACGTACTGGGACAACCTGTAACGTTGCACCTGCCAGGAGAACAGGCAGT  
GGCATGTTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG  
GAACACAGCGCCTTCTGGGGCATGACCCTGGATTGAGGGCATTTCGCTACCGCCTGGGCACCA  
TCCGCCCATCTTCTCGGTTCATGAACATGCATGAAATTTATACAGTGTGTAACCCAGGGGAG  
GTGCTTCCCACAGCCTTCGAGGCTCTGAGAAGTGCCCAACCTGATTATCATGAGCCTCTTGA  
CCAAGGCAACTGTGCAGGCTCTGGGCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT  
CAATCCATTCTCTGGGACACATGACGCTGTCTGTGCGCCAGAACCTGTGTCTTGTGAC  
ACCCACCAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTTCTGCGCTCG  
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC  
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCC  
CACTGCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCTGTCTACCGCCT  
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAAATGGCCCTGTCCAAGCCCTCA  
TGAGGTGTCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC  
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG  
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCCTGGGGCC  
CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCTGTCGCGGCGCTCAATGAGTGCGACATCGAG  
AGCTTCTGTCTGGGCGTCTGGGCGCGCTGGGCATGGAGACATGGGTCACTACTGAGGCTG  
CGGGCACCCAGCGGGGTCCGGCTGGGATCCAGGCTAAGGGCCGCGGGAAGAGGCCCAATG  
GGGCGGTGACCCAGCCTCGCCGACAGAGCCGGGGCGCAGCGGGCGCCAGGGCGCTAAT  
CCCGGCGGGGTTCCGCTGACGACGCGCCCCGCTGGGAGCCGCGGCGAGGCGAGACTGGCG  
GAGCCCCAGACCTCCAGTGGGGACGGGGCAGGGCTTGGCTTGGGAAGGACACAGCTGCAG  
ATCCCCAGGCCTCTGGCGCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC  
CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTATAGACAGGGTCTGTCTCCG  
TTGCCAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTC  
AGTGACCCCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCAACACACCTGGC  
TAATTTTTGTATTTTGTAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAACT  
CCTGGGCTCAAGCGGTCACCTGCTGCCCTCCCAAGTGCTGGGATTGCAGGCATGAGCC  
ACTGCACCCAGCCCTGTATTCTTATTCTTTCAGATATTTATTTTCTTTTCACTGTTTAAAA  
TAAACCAAAGTATTGATAAAAAA

## **FIGURE 6**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG
```

### **N-glycosylation site.**

amino acids 78-82, 161-165

### **Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

### **N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

### **Amidation site.**

amino acids 26-30, 318-322

### **Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

[illegible]

AGGCTCCTTGGCCCTTTTTCACAGCAAGCTTNTGCNATCCCGATTCTGTTGTCTCAAATCCA  
ATTCTCTTGGGACACATNACGCTGTCTTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC  
CAGCAGCAGGGGTGCGCGGNTGGGCGTCTCGATGGTGCTGTGTGGTTCCTGCGTCGCCGAGG  
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGTTCGGGGCAAGCGCCAGGCCACTGCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC  
CAACGACAAAGAGATCATGAAGGACTGATGGAGAATTGGCCCTGTCCAAGCCCTCATGGAGG  
TGACATGAGGACTTCTTCATGATACAGGTGAGGCACCTACAGCCACACGCCAGTGAGCCTTGGG  
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

## FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG  
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG  
CAGCTTGAAGTGCCTGGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT  
GCGCTGCTCCCTGCACTCGGCCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGG  
CCCCGCTGCAGCCCACACTGGGTGTGGTGCCCCAGGCCCTCTGTGCCACTCCTCACAGACCTG  
GCCCAGTGGGAGCCTGTCTGGTTCTTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCCCCACCCTGACCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA  
TCAGCTCTAGTGACACAGATCCGCCCTGCAGATGGCCCCCTCCAACCCTCTCTGCTGCTGTTT  
CATGGCCAGCATTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT  
CCCTGCCCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCAGCA  
GGGGACAGGCACTCAGGAGGGGCCAGTTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA  
GGACAAGAGTCGACGTGAGTTCTCGGGAGTCTCCAGAGATGGGGCCTGGAGGCCCTGGAGGAA  
GGGGCCAGGCCTCACATTCTGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
AATAAACACCTGTTGGATAAGCCAAAAAAA



## **FIGURE 9**

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMVYCTPVPHPDPPMALSRTPTRQISSSDT  
DPPADGPSNPLCCCFHGPAFSTLNFVLRHLFPQEAFFAHPITYDLSQVSVSVSPAPSRGQALRRAQ

### **Signal peptide:**

amino acids 1-47

### **N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

### **Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

### **N-myristoylation site.**

amino acids 56-60

### **Amidation site.**

amino acids 70-74

[illegible]

CCACACGCGTCCGAACCTCTCCAGCGATGGGAGCGCCCGCGCTGCTGCCAACCTCACTCTGTG  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGACCAGGGCGCCATGACC  
GACCAGCTGAGCAGGCGCGAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTGCAAGGTACCGGGCGCTGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC  
TCATAGTGGAGACGGACACGTTTGCGCAGCCGGGTTTCGCATCAAAGGGGCTGAGAGTGAGAAAG  
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCAGCGGGAAGAGCAAAAGACTG  
CGTGTTACCGGAGATCGTGCTGGAGAAACATATACGGCCTTCCAGAACGCCCGGCACGAGG  
GCTGGTTTCAGGCCCTTCACGCGGACGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAAC  
CAGCTCGATGGGCCCACTTCATCAAGCGCCTTACCAAGGCCAGCTGCCCTTCCCAAACACGAC  
CGAGAAGCAGAAGCAGTTTCAGTTTGTTGGGCTCCGCCCCACCCCGCGGACCAAGCGCCACAC  
GGCGGCCCCAGCCCTCAGCTAGTCTGGGAGGCAGGGGGCAGCAGCCCTGGGGCGCCTCCC  
CACCCCTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGCGCGGAGGGGAGCCAGATCCCC  
GAGGGAGGACCTTGAGGGCGCGAAGCATCCGAGCCCCAGCTGGGAAGGGGCAGGCCGGTG  
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACT  
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGGCTCCCGAGCCGGGCTCTGAAGCC  
CGCTGAAAGGTACGCGACTGAAGGCCTTGAGACAACCGTCTGGAGGTGGCTGTCTCTCAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCAGCCCCCAAACCTCCTCCTGGCTAGACTGTA  
AGGAAGGGACCTTTTGTTTGTGTTTGTTCAGGAAAAAGAAAGGGAGAGAGAGGAAAAATAG  
AAGGTTGTCCACTCTCAATTTCCACGACCCAGGCCTGCACCCACCCCCAACTCCAGCCCC  
CGGAATAAAACCTTTTCCCTGC

## **FIGURE 11**

MGAARLLPNLTLCQLLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRISATAEDGNKFALIVETDTFGSRVRIKGAESEKYICMNRGKLIKPSGKSKDCVFTEIVLENNYTAFQONARHEGWFMATFTRQGRPRQASRSRQNRQREAHFIKRLYQGQLPFPNHAEKQKQFEFVGSAPTRRTKRTRRPQPLT

### **Signal peptide:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 9-13, 126-130

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

### **Casein kinase II phosphorylation site.**

amino acids 65-69

### **Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

### **N-myristoylation site.**

amino acids 69-75, 188-194

### **Amidation site.**

amino acids 58-62

### **HBGF/FGF family signature.**

amino acids 103-128

## FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG  
GACAGCAGCAAGAGGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGGAGATTATTTTAC  
CATACGCCCTCAGGACGTTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCTATCCAGT  
CATTTTGATTTGCTGTTTATTTTTTTTCTTTTTCTTTTTCCCAACACATTGTATTTTAT  
TTCCGTACTTTCAGAAATGGGCCCTACAGACCACAAAGTGGCCCAGCCATGGGGCTTTTTTCCCT  
GAAGTCTTGGCTTATCATTTCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC  
CTAGTGTGTGCCGCTGCGACAGGAACTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG  
CCTCTTGGGATCCCGGAGGGGCTAACCGTACTCTACCTCCACAACAACCAATTAATAATGC  
TGGATTTCTGCAGAACTGCACAATGTACAGTGGTGCACACGGTCTACCTGTATGGCAACC  
AACTGGACGAATTTCCCATGAACTTCCCAAGAATGTACAGATTCTCCATTGTGCAGGAAAAC  
AATATTACAGACCATTTACGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT  
GGATGACAACCTCCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCC  
TCAAATTGTTGTTTTGTCTAAGAATCACCTGAGCAGTGTGCCCTGTTGGGCTTCCCTGTGGAC  
TTGCAAGAGCTGAGAGTGGATGAAAAATCGAATTGCTGTATATCCGACATGGCCCTTCCAGAA  
TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCTGACCAACAAGGGTATCGCCG  
AGGCGACCTTCAGCATTCTCAACCAAGCTCAAGGAATTTTCAATTGTACGTAATTCGCTGTCC  
CACCTCTCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTCAGGACCAACAGAT  
AAACCACATTCTTTGACAGCTTCTCAAATCTGCTGAAGCTGGAACGGCTGGATATATCCA  
ACAAACCACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC  
ACTGCTCGGAATAACCTTTGGTTTTGTGACTGACGTATTAATGGGTACAGAATGGCTCAA  
ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCTGAAACAAGTCCGGG  
GGATGGCCGTGAGGGAATTAATATGAATCTTTTGTCTGCCACCAAGCCTCCCGGCTG  
CCTCTCTTCACTCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACTCTCTAT  
TCCAAACCTTAGCAGAAGCTACAGCCTCCAACCTCTACCAATCGAAACTTCCCAAGATT  
CTGACTGGGATGGCAGAGAAGAGTGAACCCACCTATTTCTGAACGGATCCAGCTCTCTATC  
CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTCCACGTGATGGCATA  
CAAACTCACATGGGTGAAAAATGGGCCACAGTTTAGTAGGGGCATCGTTTCAGGACGCATAG  
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT  
TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCAGAGGC  
CACCACCCATGCCCTCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
CGTCCCACAGCATGGGCTCCCCCTTCTGTCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT  
GTGCTGGTGGTCTTGCTCAGCGTCTTTTGTGGCATATGCACAAAAAGGGGCGTACACCTC  
CCAGAAGTGGAAATACAACCGGGGCGCGCGGAAAGATGATTATTGCGAGGCGAGCACCAGA  
AGGACAACCTCATCTCTGGAGATGACAGAAACAGTTTTTCAGATCGTCTCTTAAATAACGAT  
CAACTCTTAAAGGAGATTTTCAGACTGCAGCCCATTTTACACCCCAATGGGGGCAATTAATTA  
CAGACATGCCATATCCCCAACACATGCGATATGCAACAGCAGCGTGCCAGACCTGGAGC  
ACTGCCATACGTGACAGCAGAGGCCAGCGTTATCAAGCGGACAAATTAGACTCTTGAGAA  
CACACTCGTGTGTGCACATAAAGACAGCAGATTACATTTTGATAAATGTTACAGACATGCAT  
TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG  
CTATCTTTCTATTTCAAGTTAAATACAACAGTTTTGTAACTCTTTGCTTTTTAAATCTT

## **FIGURE 13**

MGLQTTKWP SHGAFFL KSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP  
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRLHLQENNIQTI  
SRAALAQLLKLEELHLDNDSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR  
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD  
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN  
PWFCDCSIKWVTEWLKYPSSLNVRGFMCGQPEQVRGMVRELNMNLLSCPTTTPGLPLFTP  
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWGGRERVTPPISERIQLSIHFVND  
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL  
DAFNRYAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL  
LSVFCWHMHKKGRYTSQKWKYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG  
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

### **Signal peptide:**

amino acids 1-42

### **Transmembrane domain:**

amino acids 542-561

### **N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

### **Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

### **Tyrosine kinase phosphorylation site.**

amino acids 319-328

### **N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

### **Amidation site.**

amino acids 581-585

### **Leucine zipper pattern.**

amino acids 164-186

### **Phospholipase A2 aspartic acid active site.**

amino acids 39-50

# FIGURE 14

A CTCTGGAGCAAGCGGCGGCGGCGGAGACAGAGGCGAGAGGCGAGAGCTGGGGCTCCGTCCTCGCCTCCCA CGAGCG  
 ATCCCCGAGGAGAGCGCGGCCCTCGCGGAGCGAGCGAGAGGCGGCGAGGAGACCCGGGTGGCTCGGCGCCCTGCC  
 TCGCTTCCAGCGCGCGCGCGCTCGAGCCTTGCCTCTTGTCTGCCTTGAACTTGAGAAAGATGTCTCGAGGGT  
 GCTTTCTGCTATCTTCGACAGATCGTCTCTCTCTCGCGAGGCCAGGGAGCGGTCACTCGGGAGGTCCATCT  
 CTAGGGGCGACACGCTCGGACCCACCGCGAGACGGCCCTTCTGGAGAGTTCTGTGAGAAACAGCGGGCGAGACC  
 TGTGTTTTCATCATCTGACAGCTCTCGAGTGTCAACACCCATGACTATGCAAAAGGTCAAGAGATTTCATCGTGGACA  
 TCTTGCAATCTTTGGACATTTGGTCTGTATGTCAACCGAGTGGGCTGCTCCAATATGGCAGCACTGTCAAGATG  
 AGTTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGGTGGAGCGTGTCTCAAGAGGATGCGGCATCTGTCAACGG  
 GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGGAACATCGCATTTCTCAGAGAGAGAGGGGCGCGGCCCTCA  
 GGGAGATGTTGCCACGGGTTCATAATGATCGTGACAGATGGGAGACCTCAGGACTCCGCTGGCGAGGTGGTCTGCTA  
 AGGCACGGGACCGGGCATCTAATCTTTGCCATTTGGTGTGGGCGAGGTAGACTTCAACACCTTTGAAGTCCATTG  
 GGAAGTGAGCCCCATGAGGACCATGTCTTCTTGTGGCCAAATTTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC  
 AGAAGAAGTTGTGACCGGCCCATGTGTGCAGCACCTGGAGCATAAATGTGCGCCACTTCTGCATCAACATCCCTG  
 GCTCATACGTCTCGAGGTGCAACCAAGGCTACATTTCTCAACTCGGATCAGACGACTTGCAGAAATCCAGGATCTGT  
 GTGCCATGGAGGACCAACACTGTGTGAGCAGCTCTGTGTGAATGTGCGGGCTCCTTCGTCTCCAGTGTCTACAGT  
 GCTACGCGCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGAATCTGTGCGCTCAGAAAAACCGAGATGTGAAC  
 ATGATGTGTGAATGCTGATGGCTCTCACTTTGCCAGTGGCCATGAAGGATTTGCTCTTTAAACCCAGATGAAAAAA  
 CGTGACACAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGGCTCAACATGAGGAGAGGCT  
 ACTACTGCGCTGCCACCGTGGCTACACTCTGGAACCCCAATGGCAAAACCTGCAGCCGAGTGAACCATTTGTGCAC  
 AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGAGGATTCCTCTGCTGCCACGTGCTCAGAAAGCTTCC  
 TCATCAACGAGGACCTCAAGACCTGTCTCCGGGTGGATTA CTGCTCTGAGTGAACATGGTTGTGAATACTCTCT  
 GTGTCAACATGACAGATGCTTTGGCTGTGAGTGTCTCTGAGGACAGCTGCTCCGACGCGATGGGAAGACGTGTG  
 CAAAAATTTGGACTCTTGTGCTCTGGGGACCAAGGTTGTGAACATTTGCTGTGTAAGCATTTGTTGTTGTGT  
 GCCAGTGTCTTTGAAGTTTATATCTCCGTGAAGATGAAAAACCTGCAGAAAGAAAGATGTCTGCCAAGCTATAG  
 ACCATGGCTGTGAAGACATTTGTGTGAACAGTGAACGACTACACAGCTGCGAGTGTCTGGAGGAGTCCCGCTCG  
 CTGAGGATGGAAACGCTGCCGAGGAAGGATGTCTGCAAAATCAACCCACATGCTGCGCAACATTTGTGTGA  
 ATAATGGGAATTTCTACATCTGCAAAATGCTCAGAGGATTTGTTCTAGCTGAGGACGGAAGACGGTGCAGAGAAAT  
 GCACATGAAGGCCCAATTTGACCTGGTCTTTGTGATCGATGATGATGATGATGATGATGATGATGATGATGATGAT  
 TGAAGCAGTTGTCACTGGAATATAGATTTCTTTGACAAATTTCCCGCAAGGCGCTCGAGTGGGGCTGCTCCAGT  
 ATTCCACACAGGTCACACAGAGTTCACTCTGAGAAACCTTCAACTCAGCCAAAGACATGAAAAAGCGTGGCCCC  
 ACATGAAATACATGGGAAGGCGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAAGAGAGTTTACCCCAAG  
 GAGAAAGGGCGAGGCCCTTTTCAACAGGGGTGCCAGAGCAGGCAATTTGTTCACCGACGGACGGGCTCAGGATG  
 ACGTCTCCGAGTGGCGGCAATAAGCGCAAGGCCAATGGTATCATATGATGCTGTGGGGTAGGAAAAAGCCATGG  
 AGGAGGAATCAAGAGAGATGGCTCTGAGGCCCAAAACAGCATCTCTTATGCGGAAGACTTGCACCAATGG  
 ATGACATAACTGAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG  
 CAGGGCAACTGCCAAAAACGCTCCAACAGCCCAACAGAAATCTGAGCCAGTCAACATAATCCAAGACTCTATT  
 CCTGTTCTAATTTTGCAGTGCACACAGATATCTGTTTGAAGAAGCAATCTTTTACGGTCTACACAAAAGCTTT  
 CCCATTCAACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACAGATCAATGCAAAATGTGAAAAACCTTTAATGT  
 TCCGAACCTTTGCAACGAAGAAGTAAGAAAAATTACACAGCGCTTAGAAGAATGACACAGAGAATGGAAGCCCC  
 TGGAAAAATCGCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCTATTGTATCGGATTAACAT  
 GAACGCACTGACAGCCCCAAAGCTCAGGCTATTGTTAAATCAATAATGTGTGAAGTAAAAACATCAGTACTGA  
 GAAACCTGTTTGTGCCACAGAACAAAGACAAGAAGTATACACTAATCTGTATAAATTTACTAGGAAAAAATCCT  
 TCAGAAATCTTAAGATGAATTTACAGGAGTGAAGATGAATAAGCTATGCAAGGATTTTGTGAATATACCTGTGGACAC  
 AACTTGTCTTCTGCTCATCTGCTTGTGTGCAATCTCATTTGACTATACAGATAAAGTTTGCACAGCTTTACTT  
 CTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTGTACTGGACTTACCTTGATATATGATATGATGATGATGAT  
 CATAAAAATCATAGGACATATGACTTGTGGAAACAAGTTGGATTTTTTATACAAATTTAAAAATTCACACATTCAG

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## **FIGURE 15**

MEKMLAGCFLILGQIVLLPAEARERSRGRSISRGRHARTHPTQTALLESSCENKRADLVFII  
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV  
KMRHLSTGTMGLAIQYALNIAFSEAEGARPLRENVPVIMIVTDGRPDQSVAEVAAKARD  
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTLSVFQKKLCTAHMCSSTLEHN  
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA  
LAEDGKRCVADVDCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCRINYCALNKPGC  
EHECVNMEESYYCRCHRGYTLDPNGKTCSRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI  
NEDLKTC SRVDYCLLSDHGC EYSCVNMDRSFACQCP EGHVLRSDGKTC AKLDS CALDGHGCE  
HSCVSSSEDSFVCQC FEGYILREDGKTCRRKDCVQAIDHGCEHICVNSDDSYTCECLEGFRLA  
EDGKRCRRKDVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKCTEGPIDLVFVID  
GSKSLGEEFVVKQFVTGIIIDSLTISPKAARVGLLQYSTQVHTEFTLRNPNFSAKDMKKAVA  
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN  
GITMYAVGVGKAIEEELQEIASEPTNKHLYAEDFSTMDIEISEKLKKGICEALEDS DGRQDS  
PAGELPKTVQQPTESEPVTTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL  
EEKHDQCKCENLIMFQNLANEVVRKLTQRLEEMTQRMEALENRLRYR

### **Signal peptide:**

amino acids 1-23

### **N-glycosylation site.**

amino acids 221-225

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

### **Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,  
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,  
781-785, 819-823, 866-870

### **N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,  
639-645, 690-696, 752-758, 792-798

### **Amidation site.**

amino acids 314-318, 560-564, 601-605

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
540-546, 581-587

## FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCAGGCTCCGGCCGTGCGGCAGCCTCG  
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCCTGACTCCGTCCCGGCCAGGGAGGGC  
CATGATTTTCCCCTCCCGGGGCCCCCTGGTGACCAACTTGCTGCGGTTTTTGTCTCTGGGGCTGA  
GTGCCCTGCGCCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCCCAACCGGTTGCAG  
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGAGGTGTCTTTC  
ATCCAGCCATGGGAGGTGCCCTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC  
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA  
CAGCTGCTCCGTGAATGTGAAGACAAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT  
TAGAACTCAATGTACTGGTTCCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT  
GTGGGGGCAACGCTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTCTTTGCACCAGCATTAGATGTCTATCCGTG  
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC  
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC  
AGTGGTTGCTGGAGCTGTTGTGGGTACCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC  
TCTTGTACCACCGCCGGGCAAGGCCCTGGAGGAGCCAGCCCAATGATATCAAGGAGGATGCC  
ATTGCTCCCCGGACCCTGCCCTGGCCCAGAGCTCAGACACAATCTCCAAGAATGGGACCCT  
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCAT  
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACAGACAGAT  
GGGGCCCAACCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCG  
CATGGGTGCTGTGCTGTGATGGTGCTGCCAGAGTCAAGCTGGCTCTCTGGTATTGATGCAC  
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACCTCTAGCAC  
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCCACTCTC  
TTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG  
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGC  
CCCCCTGATCTGTACCCCAACCCCTATCTAACACCACCTTGGCTCCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTCAAGGCTGGCTTGGTTAGGTTTTTACTGGGGCAGAGGATAGGGAATCTC  
TTATTAAAACATAACATGAAATATGTGTTGTTTTTATTGCAAATTTAAATAAAGATACATAA  
TGTTTGTATGAAAAA



Reaction	Time (h)	Yield (%)	Structure
1a + 2a	24	85	3a
1b + 2b	24	80	3b
1c + 2c	24	75	3c
1d + 2d	24	70	3d
1e + 2e	24	65	3e
1f + 2f	24	60	3f
1g + 2g	24	55	3g
1h + 2h	24	50	3h
1i + 2i	24	45	3i
1j + 2j	24	40	3j
1k + 2k	24	35	3k
1l + 2l	24	30	3l
1m + 2m	24	25	3m
1n + 2n	24	20	3n
1o + 2o	24	15	3o
1p + 2p	24	10	3p
1q + 2q	24	5	3q
1r + 2r	24	0	3r

Signal peptide:

Transmembrane domain:

N-glycosylation site.

N-myristoylation site.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

[illegible]

## **FIGURE 19**

MKRLPELLVVFFSTLLNCSYTNCTKTPLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC  
GNLTQSCGENANCNTNTEGSSYYCMCVPGFRSSSNQDRFITNDGTVCIEVNVNANCHLDNVCIAA  
NINKTTLKIRSIKEPVALLQEYVRNSVTDLSPTDIIITYEILAESSLLGYKNNTISAKDTL  
SNSSTLTBFVKTVNNFVQRDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSFOKTTTFPDT  
NSTDIALKVVFFDSYNMKHIHPHMNMMDGDYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS  
SSDNFLLKPNQYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTTLSHRKVTDYRSLCAF  
WNYSPTDMNGSWSSGCELTYSNETHTSCRCNHLTHFAILMSSGSPSIGIKDYNILTRITQLG  
IIISLICLAICITFTWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIIAGL  
LHYFFLAFAWMCIEGHIHLYLVVGVYINKGFLHKNFYIFGYLSPAVVVGFSAAALGYRYYGT  
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRTAGLKPEVSCFENIRSCARGA  
LALLFLGLTTWIFGVLHVHVASVVTAYLFTVSNAPQGMFIFLFLCVLSRKIQEEYRLFKNV  
PCCFGCLR

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,  
648-664

**N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

**Glycosaminoglycan attachment site.**

amino acids 49-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

**Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

**Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

**N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

**Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

	(a)	(b)	(c)	(d)	(e)	(f)	(g)	(h)	(i)	(j)	(k)	(l)	(m)	(n)	(o)	(p)	(q)	(r)	(s)	(t)	(u)	(v)	(w)	(x)	(y)	(z)	(aa)	(ab)	(ac)	(ad)	(ae)	(af)	(ag)	(ah)	(ai)	(aj)	(ak)	(al)	(am)	(an)	(ao)	(ap)	(aq)	(ar)	(as)	(at)	(au)	(av)	(aw)	(ax)	(ay)	(az)	(ba)	(bb)	(bc)	(bd)	(be)	(bf)	(bg)	(bh)	(bi)	(bj)	(bk)	(bl)	(bm)	(bn)	(bo)	(bp)	(bq)	(br)	(bs)	(bt)	(bu)	(bv)	(bw)	(bx)	(by)	(bz)	(ca)	(cb)	(cc)	(cd)	(ce)	(cf)	(cg)	(ch)	(ci)	(cj)	(ck)	(cl)	(cm)	(cn)	(co)	(cp)	(cq)	(cr)	(cs)	(ct)	(cu)	(cv)	(cw)	(cx)	(cy)	(cz)	(da)	(db)	(dc)	(dd)	(de)	(df)	(dg)	(dh)	(di)	(dj)	(dk)	(dl)	(dm)	(dn)	(do)	(dp)	(dq)	(dr)	(ds)	(dt)	(du)	(dv)	(dw)	(dx)	(dy)	(dz)	(ea)	(eb)	(ec)	(ed)	(ee)	(ef)	(eg)	(eh)	(ei)	(ej)	(ek)	(el)	(em)	(en)	(eo)	(ep)	(eq)	(er)	(es)	(et)	(eu)	(ev)	(ew)	(ex)	(ey)	(ez)	(fa)	(fb)	(fc)	(fd)	(fe)	(ff)	(fg)	(fh)	(fi)	(fj)	(fk)	(fl)	(fm)	(fn)	(fo)	(fp)	(fq)	(fr)	(fs)	(ft)	(fu)	(fv)	(fw)	(fx)	(fy)	(fz)	(ga)	(gb)	(gc)	(gd)	(ge)	(gf)	(gg)	(gh)	(gi)	(gj)	(gk)	(gl)	(gm)	(gn)	(go)	(gp)	(gq)	(gr)	(gs)	(gt)	(gu)	(gv)	(gw)	(gx)	(gy)	(gz)	(ha)	(hb)	(hc)	(hd)	(he)	(hf)	(hg)	(hh)	(hi)	(hj)	(hk)	(hl)	(hm)	(hn)	(ho)	(hp)	(hq)	(hr)	(hs)	(ht)	(hu)	(hv)	(hw)	(hx)	(hy)	(hz)	(ia)	(ib)	(ic)	(id)	(ie)	(if)	(ig)	(ih)	(ii)	(ij)	(ik)	(il)	(im)	(in)	(io)	(ip)	(iq)	(ir)	(is)	(it)	(iu)	(iv)	(iw)	(ix)	(iy)	(iz)	(ja)	(jb)	(jc)	(jd)	(je)	(jf)	(jg)	(jh)	(ji)	(jj)	(jk)	(jl)	(jm)	(jn)	(jo)	(jp)	(jq)	(jr)	(js)	(jt)	(ju)	(jv)	(jw)	(jx)	(jy)	(jz)	(ka)	(kb)	(kc)	(kd)	(ke)	(kf)	(kg)	(kh)	(ki)	(kj)	(kk)	(kl)	(km)	(kn)	(ko)	(kp)	(kq)	(kr)	(ks)	(kt)	(ku)	(kv)	(kw)	(kx)	(ky)	(kz)	(la)	(lb)	(lc)	(ld)	(le)	(lf)	(lg)	(lh)	(li)	(lj)	(lk)	(ll)	(lm)	(ln)	(lo)	(lp)	(lq)	(lr)	(ls)	(lt)	(lu)	(lv)	(lw)	(lx)	(ly)	(lz)	(ma)	(mb)	(mc)	(md)	(me)	(mf)	(mg)	(mh)	(mi)	(mj)	(mk)	(ml)	(mm)	(mn)	(mo)	(mp)	(mq)	(mr)	(ms)	(mt)	(mu)	(mv)	(mw)	(mx)	(my)	(mz)	(na)	(nb)	(nc)	(nd)	(ne)	(nf)	(ng)	(nh)	(ni)	(nj)	(nk)	(nl)	(nm)	(nn)	(no)	(np)	(nq)	(nr)	(ns)	(nt)	(nu)	(nv)	(nw)	(nx)	(ny)	(nz)	(oa)	(ob)	(oc)	(od)	(oe)	(of)	(og)	(oh)	(oi)	(oj)	(ok)	(ol)	(om)	(on)	(oo)	(op)	(oq)	(or)	(os)	(ot)	(ou)	(ov)	(ow)	(ox)	(oy)	(oz)	(pa)	(pb)	(pc)	(pd)	(pe)	(pf)	(pg)	(ph)	(pi)	(pj)	(pk)	(pl)	(pm)	(pn)	(po)	(pp)	(pq)	(pr)	(ps)	(pt)	(pu)	(pv)	(pw)	(px)	(py)	(pz)	(qa)	(qb)	(qc)	(qd)	(qe)	(qf)	(qg)	(qh)	(qi)	(qj)	(qk)	(ql)	(qm)	(qn)	(qo)	(qp)	(qq)	(qr)	(qs)	(qt)	(qu)	(qv)	(qw)	(qx)	(qy)	(qz)	(ra)	(rb)	(rc)	(rd)	(re)	(rf)	(rg)	(rh)	(ri)	(rj)	(rk)	(rl)	(rm)	(rn)	(ro)	(rp)	(rq)	(rr)	(rs)	(rt)	(ru)	(rv)	(rw)	(rx)	(ry)	(rz)	(sa)	(sb)	(sc)	(sd)	(se)	(sf)	(sg)	(sh)	(si)	(sj)	(sk)	(sl)	(sm)	(sn)	(so)	(sp)	(sq)	(sr)	(ss)	(st)	(su)	(sv)	(sw)	(sx)	(sy)	(sz)	(ta)	(tb)	(tc)	(td)	(te)	(tf)	(tg)	(th)	(ti)	(tj)	(tk)	(tl)	(tm)	(tn)	(to)	(tp)	(tq)	(tr)	(ts)	(tt)	(tu)	(tv)	(tw)	(tx)	(ty)	(tz)	(ua)	(ub)	(uc)	(ud)	(ue)	(uf)	(ug)	(uh)	(ui)	(uj)	(uk)	(ul)	(um)	(un)	(uo)	(up)	(uq)	(ur)	(us)	(ut)	(uu)	(uv)	(uw)	(ux)	(uy)	(uz)	(va)	(vb)	(vc)	(vd)	(ve)	(vf)	(vg)	(vh)	(vi)	(vj)	(vk)	(vl)	(vm)	(vn)	(vo)	(vp)	(vq)	(vr)	(vs)	(vt)	(vu)	(vv)	(vw)	(vx)	(vy)	(vz)	(wa)	(wb)	(wc)	(wd)	(we)	(wf)	(wg)	(wh)	(wi)	(wj)	(wk)	(wl)	(wm)	(wn)	(wo)	(wp)	(wq)	(wr)	(ws)	(wt)	(wu)	(wv)	(ww)	(wx)	(wy)	(wz)	(xa)	(xb)	(xc)	(xd)	(xe)	(xf)	(xg)	(xh)	(xi)	(xj)	(xk)	(xl)	(xm)	(xn)	(xo)	(xp)	(xq)	(xr)	(xs)	(xt)	(xu)	(xv)	(xw)	(xx)	(xy)	(xz)	(ya)	(yb)	(yc)	(yd)	(ye)	(yf)	(yg)	(yh)	(yi)	(yj)	(yk)	(yl)	(ym)	(yn)	(yo)	(yp)	(yq)	(yr)	(ys)	(yt)	(yu)	(yv)	(yw)
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TGGAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAGNG  
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT  
TGGTCCCTTTGCTTTTCATCATCTGACAACTTCTTATTGAAACCTCAAATTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCCACCAC  
ATTATATGAACCTGAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATA  
GGAGTCTATGTGGCATTTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGCATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTTGCAATTTTGATGTCCTCTGGTCTTCCATTGGTATTAAAGATTATAATATCTTACAA  
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTACCTTC  
TGGTCTTCAGTGAAATTCAAAGCACCAGGA

## FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG  
CTAAGCGAGGGCTCTCTCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCGGCTGGGA  
CAAGAAGCCGCCGCTGCTGCGCCGGGCCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG  
GGTGTAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG  
TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCGGAG  
CCGCCGCGCCGTGAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC  
GGCACTCACAGCCCGCAGCGCATCCCGGTGCGCCGCCAGCCTCCCGACCCCCATCGCCGG  
AGTTCGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG  
ATCCTGGCCGGCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC  
CCACGTGCATACGGCTGGGGCGACCCCATCCGCCGTGCGGCACCTGTACACCTCCGGCCCCC  
ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTGTGGACTGCGCGCGGGGC  
CAGAGCGCGCACAGTTGTGAGATCAAGGCAGTCCGCTCTGCGGACCGTGGCCATCAAGGG  
CGTGCACAGCGTGGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA  
TCCGAGAAGCACCCGCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA  
CAGAGGCTTCTTCCACTCTCTATTTCCTGCCCATGCTGCCCATGGTCCAGAGGAGCCTG  
AGGACCTCAGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCTGGAGACCCGACAGCATG  
GACCCATTGTGGCTTGTACCCGGAAGTGGAGGCCGTGAGGAGTCCACGCTTTGAGAAGTAAC  
GAGACCATGCCCGGGCCTCTTCACTGTGTCAGGGGCTGTGGTACCTGACGCTGGGGGACG  
TGCTTCTACAAGAACAGTCTGTAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA  
GTTGTACATATTCAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAAATAGACTTGTCTGAT  
CATAACATTGTAAGCTGTAGCTTGCCAGCTGCTGCTGGGGCCCCATTCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGTGCACTGTCTCAGTTCGTCTGAATACTCCATCGATGGGGAAC  
TCACTTCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTCTCATCACTTC  
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTAGGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG  
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAAGTCACTGGAGCAGGCATGGCCACCAG  
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACTTGAGAATTTCCC  
CTGAGGCCAGTTCTGTGATGGATGCTGTCTGAGAATAACTTGCTGTCCCGGTGTCACTGTC  
TTCATCTCCAGCCCAACAGCCCTTGCCCACTCACATGCTCCCATGGATTGGGGCCT  
CCCAGGCCCCCACTTATGTCAACCTGCACCTTCTGTTCAAAAATCAGGAAAAGAAAGAT  
TTGAAGACCCCAAGTCTTGTCAATAACTTGTGTGTGAAGCAGCGGGGGGAACCTAGAAC  
CCTTTCCCAGCACTTGGTTTTTCAACATGATATTTATGAGTAATTTATTTTGATATGTACA  
TCTCTTATTTCTTACATTATTTATGCCCCAAATTATATTATGTATGTAAGTGAGGTTTG  
TTTTGTATATATAAATGGAGTTTGTTTGT

## **FIGURE 22**

MRSGCVVHVWILAGLWLA VAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLEIKA VALRTVAIKGVHSVRYLCMGADGKMQLLYSEEDCAFEE  
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPPEPEDLRGHLESD  
MFSSPLETDSMDPFGGLVTGLEAVRSPSFEK

### **Signal peptide:**

amino acids 1-22

### **Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

### **N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

## FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTCGACCTCCTCA  
GAGCAGCCGGCTGCCGCCCCGGGAAGATGGCGGAGGAGAGCCGCCACCGCCTCCTCCTGCTG  
CTGCTGCGCTACCTGGTGGTGCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCCAAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA  
AGAAGACTGTTTCCTCCAGATTAGAGTGGAAGAACTGGGTGGAGTGTCTCCTTTGTCTAC  
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCAGCTGAGATGATAGATTTCAATATCCG  
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCATCTG  
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAAGGATGGCATCCGTTTGCTAGAAA  
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATAACAATGAATACAAAACTGGAAGT  
CTGCAATTTAATACTGTTTCCAACTGGACACTGGAGAATATTCTGTGAAGCCCGCAATTC  
TGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA  
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT  
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATTTCTCATCTAA  
AGCCACGACAATGAGTGAAAAATGTGCAGTGGCTCACGCCTGTAATCCAGCACTTTGGAAGG  
CCGCGGCGGGCGGATCACGAGGTGAGGAGTTCAGACCACTCTGGCCAATATGGTGAAACCC  
CATCTCTACTAAAATACAAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC  
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGGTAAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAATA  
AATAAATACTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

## **FIGURE 24**

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE  
WKKLGRSVSVFVYYQQTLOGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEED  
TVTLEVLVAPAVPSCSEVPSSALSGTIVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST  
NSSYTMNTKTGTQLQFNTVSKLDTGEYSCEARNVSGYRRCFPGKRMQVDDLNI SGIIA AVVVVA  
LVISVCGLGVCYAQRKGYFSKETS FQKSNSSSKATTMSENVQWLTPVIPALWKAAGGSRGQEF

### **Signal peptide:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 130-144, 238-258

### **N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

### **Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

### **N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

### **Amidation site.**

amino acids 226-230



## FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG  
AAAGAAGAGGAAGATGTTGGGGCAACATTATTTAAACATGCTCCACAGCCCGGACCCCTGGCAT  
CATGCTGCTATTCTCTGCAAAATCTGAAGAAGCATGGGATTTAAATATTTTACTTCTTAAATAA  
ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTTCAAAGTACATCAATA  
TTATATCATTAAAGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTTTGGACAATG  
CAATTGTGGCACTGGCATTATTTTCAGTGAAGAAAACTTTGGTGTCTATGGCATTTCATCA  
TTTGACAAATGCAAGCATCTTCTTATCAATCAGCTCCTATTGAACCTTACTAGCACTGACTG  
TGGAACTCCTTAAGGGCCCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT  
CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG  
TGGATTGTCACGGTTATGTACGTGTGAAATCAGGCCTTGGTTTACACCCAGATCCATTAT  
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCCTTTAACTTTCCACGCCAGATTGCC  
AGCTAACACACAGATTCTTCTCCTACAGACTAACAAATATTGCAAAAAATGAATACTCCACAG  
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTTATCTTCAGTCACCAAT  
ATTAATGTAAAAAAGATGCCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAAACAACTTACTGA  
ACTGCCCTGAAAAATGCTGTCCGAACCTGAGCAACTTACAAGAACTCTATATTAATCACAACT  
TGCTTTTCAAAATTTCTCCTGGAGCCTTTATTGGCCCTACATAATCTTCTTCGACTTCATCTC  
AATTCAAATAGATTGCAGATGATCAAAGTAAAGTGGTTTGTAGTCTTTCCAAATCTAGATCA  
TCTGTATGATTGGGGAAAAATCCAATTATCAGAATCAAAGACATGAACCTTAAAGCCTTATCA  
ATCTTCGCAGCCTGGTTTATAGCTGGTATAAACCTCAAGAAAATACCAGATAACGCCTTGGTT  
GGACTGGAATACTAGAAAGCATCTCTTTTACGATAACAGGCTTATTAAAGTACCCCATGT  
TGCTCTTCAAAGAGTTGTAATCTCAAATTTTGGATCTAAATAAAAAATCCTATTAATAGAA  
TACGAAGGGGTGATTTAGCAATATGCTACACTTAAAGAGTTGGGGATAAATAATATGCCT  
GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTAAAGAAAAATAGAAGC  
TACTAACACCCCTAGATTGTCTTACATTCACCCCAATGCATTTTTCAGACTCCCCAAGCTGG  
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATTGGTACCATTGAGTCTCTG  
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTCAATCCGTTG  
GATGAACATGAACAAAAACCAACATTGATTCATGGAGCCAGATTCACCTGTTTTCGCTGGACC  
CACCTGAATTCCAAGGTGAGAATGTTTCGCAAGTGCAATTTTCAGGGACATGATGGAATTTGT  
CTCCCTCTTATAGCTCCTGAGAGCTTCTCTCTAATCTAAATGTAGAAGCTGGGAGCTATGT  
TTCCTTTCACTGTAGAGCTACTGCAGAACCACAGCCTGAAATCTACTGGATAACACCTTCTG  
GTCAAAACCTCTTGCTTAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA  
GATATAAATGGCGTAACCTCCCAAAGAGGGGTTTATATACCTGTATAGCAACTAACCTAGT  
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG  
GCTCTTTTGAATATTAAATAAGAGATATTCAGGCCAATTTCAGTTTGGTGTCTGGAAAGCA  
AGTTCTTAAATCTCAAAATCTAGTGTAAATGGACAGCCTTTGTCAAGACTGAAAAATCTCA  
TGCTGCGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC  
CATCAACTGAGTATAAAATTTGTATTGATATCCACCATCTATCAGAAAAACAGAAAAAA  
TGTGTAATGTCAACCAAAAGGTTTTCACCCCTGATCAAAAGAGTATGAAAAAGAAATAATC  
CACAACTTATGGCCTGTCTTGGAGGCCCTTCTGGGGATTATTTGGTGTGATATGTCTTATCA  
GCTGCCCTCTCCAGAAATGAACCTGTGATGGTGACACAGATTTGGAGGAATTAATTAACAG  
AAACCAACCTTTGATATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAA  
AGAAAAAGTACATCACTGAAAGTAAAGCACTGTTATAGGTTTACCAACAATATGTCTT  
AAAAACCAACAAGAAACCTTACCAAAATGAAC

## FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTTPRSIYMEASTVDCNDLGLLT  
FPARLPANTQIILLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE  
ENKLTTELPEKCLSELNLQELYINHNLSTISPGAFIGLHNLRLHLNSNRLQMINSKWFDA  
LPNLEIILMIGENPIIRIKDMNFKPLINLRSVIAGINLTIIPDNALVGLENLESISFYDNRL  
IKVPHVALQKVNNLKFLDLNKNPINRIRRGDFSNNMLHLKELGINNMPELISIDSLAVDNLPD  
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHGTTIESLPNLKEISIHSPIRC  
DCVIRWMNMNKTNIREFMEPDSLFCVDPPEFQGNVRQVHFRDMMEICPLIAPESFPSNLNV  
EAGSYVSFHCRTAEFPQPEIYWITPSGQKLLPNTLTDKIFYVHSEGTLDINGVTPKEGGLYTC  
IATNLVGADLKSVMIKVDGSFPQDNNGSLNLIKIRDIQANSVLVSWKASSKILKSSVKWTAFV  
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE  
YEKNNTTTLMACLGGLGIIGVICLISCLSPENMCDGGHSYVRNYLQKPTFALGELYPLIN  
LWEAGKEKSTSLKVKATVIGLPTNMS

### Signal sequence:

amino acids 1-22

### Transmembrane domain:

amino acids 633-650

### N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

### Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

### Tyrosine kinase phosphorylation site.

amino acids 570-579

### N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

### Cell attachment sequence.

amino acids 277-280

## FIGURE 27

GCCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAAACCTTTAC  
CAGCCTTGTGTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGC**ATGA**AATCT  
GGTAGACCTGTGGTTAACCCTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTGTTCCTTA  
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCCTCCTCTGGG  
GGTTTAAATGTACCTGTAGCAATGCAAACTCTCAAGGAAATACCTAGAGATCTTCCTCCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTTAAGG  
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT  
GCCTTCAAAGGAGTAGCTGAAACCTTGCCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG  
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAAACCCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCAC  
AACGTGATCTGTAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCCTCAATGCTGC  
CAACGACGCTGACCTTTGTAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTTTGGCTGGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG  
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGTAT**TAG**TGTCCAACTGACTGTCAATTGAGAAAGAAAGAAA  
GTAGTTTGCATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAA  
ACTTTGTATTTCAGTTTTTTTTGAATTATGCCACTGCTGAACTTTTAACAAACACTACAACA  
TAAATAATTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT  
AATTTAAAGCAAATAAAAGCTTAACCTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

[illegible]

Signal sequence:

Transmembrane domain:

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

**Figure 1** *Flowchart illustrating the selection of the study population*

ACCGAGCCGAGCGGACCGAAGGCGCGCCGAGATGCGAGGTGAGCAAGAGGATGCTGGCGGG  
 GCGCTGAGGAGCATCTCCGAGCCCTCTCGGCTGTGCGAGCCATCTCTGCTGGTGGT  
 GGCGTCAGTGTCTGAGGCTCGGCCAGGGCTGCCCGCGCTGCGATGCTCCGCGGAGT  
 ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCGGAGGGCATCCCCACGAG  
 ACGCGCTCTGTGAGCTAGGCAAGAACCGCATCAAAACGCTCAACAGGACGAGTGTCCGACG  
 CTTCCGCACTGTGGAGGAGTGCGAGCTCAACGAGAACATCTGAGCGCGGTGGAGCCCGCGC  
 CTTTCAACAACACTTCTCAACCTCCGAGCGCTGGGTCTCCGACGCAACCGCCTGAAGCTCAT  
 CCGTAGGCGCTTTCATCGGCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGAT  
 CGTTATCTTACTGACTACATGTTTCAGGACCTGTACAACTCAAGTCTGTGAGGTGTGGC  
 ACAATGACCTCGTCTACATCTCTCACCGCGCTCTCAGCGGCTCAACAGCCTGGAGCAGCTG  
 ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACGAGGCGTGTCCCACTGACGGCCT  
 CATCGTCTCGAGGCTCGGCCACTCAACATCAATGCCATCCGGGACTACTCTTCAAGAGGC  
 TGTACCGACTCAAGGTTCTTGAGATCTCCCACTGGGCCCTACTTGGACACCATGACAACCAAC  
 TGCTCTACGGCCTCAACTCGTAGCTCCCTGTCCATCACACATGCAATCTGACCGCTGTGCC  
 CTACCTGGCGCTCGGCCACTAGTCTATCTCGGTTCTCAACCTCTCCTCAACCAACCTCA  
 GCACACTTATGAGGCTCATGTTGTCATGAGCTGCTCGCGCTGAGCGAGGATCAGCTGTGTGGC  
 GGGCAGCTGGCGCTGTGTGGAGCCATAGCTCTCGCGGCTCAACTACTGCGCGTGCTCAA  
 TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGTGGGCAACTG  
 AGACACTCTGCTTGAGACTCAACCCGCTGCGCTCGCATCTGTGGCTCTGTGGTGTGTTCCG  
 CGCGCTCGCGGCTCAACTTCAACCGGCGAGCAAGCCAGTGGCGCACCGCCGAGTTGTGCA  
 GGGCAAGGAGTCAAGGACTTCCCTGATGTCTACTGCCCACTACTTCACTCGCGCGCGG  
 CCGCATCCGGGACCGCAAGGCGCCAGCGGTGTTTGTGACAGGGGCCACAGGTGCAAGT  
 GTGTGCGGGCGGATGGCGACCGCGCCCGCATCTCTGTGCTTCAACCCGAAGACACT  
 GGTCTCAGGCAAGGACGATGGGCGGCTCAGAGTCTCCCTGATGGCACGCTGGAGGTGCGCT  
 ACGCCAGGTACAGGACAACGGCAGCTACTGTGATCTCGGGCCAGCGGCGGCGCAAGCA  
 TCCATGCCCGCCACCTGTGATGTGGCGAGTACTCGCCGATGGCCCCATCGGCCAACAA  
 GACTCTCGCTTTCATCTCAACACAGCGCGGCGAGGAGAGGCCAACAGCCACCGCGCACT  
 TGCTTTTCCCTTTCAGATCAAGAGCTCATCATCGCCACCACTAGGCTTTCATCTCTTTC  
 CTGGGCGTGTCTCTTCTGCTGTGGTGTGCTGTTTCTGTGGAGCCGGGGCAAGGGCAACAC  
 AAAGCAACAACCTCGAGATCGAGTATGTGCCCGAAAGTCGGAAGCAGGACATCAGCTCGCGC  
 ACGCGCCCGCAAGTTCAACATGAGATGATATGAGCGCCGGGCGGGGCGAGGCCACCCG  
 GCGCGCGGGCGAGGGGAAGGGGCTGGTGCACCTGCTCACTCTCCAGTCTCTCCACCTC  
 CTCCTACCTCTTACACACGTTCTCTTCTCCCTCCGCGCTCGGCTCCCTGCTGCCCCCG  
 CGAGCCTCACCACTGCCCTCTTCTTACAGGACCTCAGAAGCCAGACCTGGGGACCCCA  
 CTTACACAGGGCGATGACAGACTGGAGTGTGAAGCCGACGAACCGACACGCGGCAGAGTCA  
 ATAATTCAATAAAAAAGTTACGAATTTCTGTAACTTTGGGTTTCAATAATTATGATTTT  
 TATGAAAACTGAAATAATAAAAAAGAAAAAACTAAAAAAAATAAAAAAAA

## **FIGURE 30**

MQVSKRMLAGGVRSMPSPLLACWQPIILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCF  
VAVPEGIPTETRLDDLGNRIKTLNQDEFASFPHLELELNENIVSAVEPGAFNNLFNLRTL  
GLRSNRRLKLIPLGVFTGLSNLTQDI SENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA  
FSGLSNLEQLTLEKCNLTSTIPTALSHLHGLIVLRLRHLNINAI RDYSFKRLYRLKVLEISH  
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLEH  
LRLQBIQLVGGQLAVVEPYAFRGLNLYLRVLNVSGNQLTTLLEESVFHSGVGNLETLILDSNPLA  
CDCRLLWVFRRLWRLNFRQOPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDPPIAILWLSPRKHLVSAKSNGRLTVPFDGTLVRYAQVQDNGTYL  
CIAANAGGNDSPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI  
IATTMGFISFLGVVLFCLVLLFLWSRGKNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 556-578

### **N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

### **Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

### **Tyrosine kinase phosphorylation site.**

amino acids 590-598

### **N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

# FIGURE 31

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAAC  
 ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGGATTGAGGCTCGCCAGCGCCAGCC  
 AGGGAGCCGGCCGGGAAGCGCGATGGGGGGCCCCAGCCGCTCGTCTCTGCTCCTGCTCCTGC  
 TGTTCGCTGCTGCTGGGCGCCCGCGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG  
 ACATCTGATGAAAAGTGGTGGCTGGTGGCACCGTGGTGTCAAGTGCCAAAGTGAAAGATCA  
 CGAGGACTCATCCCTGCAATTGAGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA  
 GAGCCCTTCGAGATAATCGAATTGAGTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC  
 ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT  
 CGGAATGCGCAAGTCCCTCGTCACTGTGCTAGGAATTCACAGAACCCATCATCACTGGTT  
 ATAAATCTTATTACGGGAAAAAGACACAGCCACCCTAAACTGTCAGTCTTCTGGGAGCAAG  
 CCTGCAGCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT  
 ACAGGAAGATCCCAATGGTAAAAACCTTCACTGTCAGCAGCTCGGTGACATTCAGGTTACCC  
 GGGAGGATGATGGGGCGAGCATCGTGTCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC  
 AGATCCACCTCTCAACGCATTGAAGTTTTATACACCAACTGCGATGATTAGGCCAGACCC  
 TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGTACTACTGTGAGGGTCGCGGCAATCCAGTCC  
 CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
 GCCCTGATCTTCCCTTTCTCTAACAGAGTGACAGTGGCACCTACGGTGCACAGCCACCAG  
 CAACATGGGCAGCTACAAGGCCTACTACACCTCAATGTTAATGACCCAGTCCGGTGCCCT  
 CCTCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCAATTGTCTTCTGCTG  
 CTCATCATGCTCATCTTCTTGGCCACTACTGATCCGCGCACAAAGGAACCTACCTGACACA  
 TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG  
 GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTATCTAGAGGCGCTGCCACTTCTCTGC  
 GCCCCCAGGGGCCCTGTGGGGACTGTGGGGCCGTACCAACCCGGCACTTGTACAGAGCAA  
 CGCAGGGCCGCCCCCTCCCGCTTGTCTCCCAGCCACCCACCCCTGTACAGAATGTCTGC  
 TTTGGGTGCGGTTTTGTACTCGGTTTGGAAATGGGGAGGGAGGAGGGCGGGGGAGGGGAGGG  
 TTGCCCTCAGCCCTTTCGTGGCTTCTCTGCATTGGGTTATTATTATTTTGTAAACAATCC  
 CAAATCAAATCTGTCTCCAGGTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA  
 AACAAAAACA

## **FIGURE 32**

MGAPAASLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW  
SNPAQQTLYFGBKRALRDNRILVLTSTPHELSSISISNVALADEGEYTCSTFTMPVRTAKSLV  
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQE DPNGK  
TFTVSSSVTFQVTRDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ  
KLLLHCEGRGNFVPQQYLWEKEGVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA  
YYTLNVNDPSPVSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIIRHKGTYLTHEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 331-352

### **N-glycosylation site.**

amino acids 25-29, 290-294

### **Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

### **N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18



## FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTTTCTTCTCCTTTCCTGG  
 CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG  
 TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT  
 GCTGGAGACGCTCTCTTTGTTTTGCGCTGGAACGTTACAGGGGACGTTTGCAAGAGAGA  
 TCTGTTCTGCAATGAGATAGAGGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACA  
 AGCTCGACGGCTTCACTGCCCGGACTTCCGAGTTTACCATTATTTCTGCAATGGCAATTTC  
 CCTCACCTGCATTTTCCCTAAATGAGTTTCGCTAACTTTTATAATGCGGTTAGTTTGCAATGG  
 AAAACAATGGCTTGCATGAATCGTTCCGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAGG  
 CTGCACATCAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA  
 TCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATATAGACCCGGGGGCTTCCAGG  
 ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCTTACCTGCCAAC  
 GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAACGCTGCC  
 CTATGAGGAGTCTTGGAGCAAATCCCTGGTATTGTCGGGAGATCCTGCTAGAGGATAACCCCTT  
 GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAAACATCCCAAGAATGCC  
 CTGATCGGCCGAGTGGTCTGCGAAGCCCCACAGACTGCAGGTAAGACCTCAATGA AAC  
 CACCGAACAGGACTTGTGTCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGCGCCCCCTG  
 CCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAATCTTTTCAAGACAATGGGCAAGAG  
 GATCATGCCACACAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCGAGCAACTGGGAGAT  
 CAAAAACAGACCCACAGCAGCGATAGCGAGGGTAGCTCCAGGAACAAACCTTAGCTTAACA  
 GTTTACCTGCCCCGGGGCTGCAGCTGCGACCACATCCAGGGTTCGGGTTTAAAGATGAAC  
 TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCCAAGCTCTCTAACGTGCAGGA  
 GCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTTGTGGATTACAAGA  
 ACCTCATTTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACTTTCAAG  
 AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACAGCTGTCCCGGGA  
 GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAAACGTGGAGTACAAAGCTATCCAGCTCA  
 TCCTCCCGGGCACTTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAACAACCTG  
 CTGAGGTCCCTGCGCTGTGGACGTGTTGCTGGGGTCTCGCTCTCTAAACTCAGCCTGCACAA  
 CAATTACTTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA  
 TAGACCTCCACGGGAACCCCTGGGAGTGCTCCTGCACAATTGTGCCCTTCAAGCAGTGGGCA  
 GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTCTT  
 TAGAAAGGATTTATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT  
 CGCCACGTTAACTTCGCAAGTAAAAACAGCAGCTGGGTTGGCGGAGACCGGACGCACTCC  
 AACTCCTACCTAGACACCAAGCAGGGGTGCTCATCTCGGTGTTGGTCCCGGGACTGCTGCTGGT  
 GTTTGTCACTCCGCCCTTACCCTGGTGGGCACTGCTCGTGTATTCTCTGAGGAACCGAAAGC  
 GGTCCAAAGAGACGAGATGCCAATCTCCGCGTCCGAGATTAATCCCTACAGACAGCTGTG  
 GACTCTTCTACTGGCACAATGGGCCCTTACAACGAGATGGGGCCACAGAGTGTATGACTG  
 TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGGAGGCGAGGGGAAGGCG  
 ATACATCCTTCCCCACCGCAGGCACCCCGGGGGCTGGAGGGCGGTATACCCAAATCCCCGCG  
 CCATCAGCCTGGATGGGCAATAAGTAGATAAATAACTGTGAGCTCGCACACCCGAAAGGGCCCT  
 GACCCCTTACTTAGCTCCTCTTGAACAAGAGCAGACTGTGGAGAGCTGGGAGAGCTGCAAGC  
 GCCAGCTCGCTCTTTGCTGAGAGCCCTTTTGACAGAAAGCCAGCAGCAGCCCTGCTGGAAG  
 AACTGACAGTGCCCTCGCCCTCGGCCCCGGGGCTGTGGGGTTGGATGCGCGGTTCTATAC  
 ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTCCCTGTGGATTAG  
 CCCCCTGATGGCTCCTGTGGCTACGAGGGATGGCAGTTGCACGAAGGCATGAATGTAT  
 TGTAATAAGTAACCTTTGACTTCTGAC

## FIGURE 34

MLLWILLLETSLCFAAGNVTGDEVCKEIKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTQSQFYH  
LFLHGNSLTRLPNEFANFYNAVSLHMENGLHEIVPGAFLGLQLVKRLHINNKKISFRKQ  
TFLGLDDLEYLQADFNLLRDIDPGAQFDLNKLEVLILNDNLISTLPANVFQYVPI THLDLRG  
NRLKTLPEYEEVLEQIPGIAETILLEDNPDWCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ  
GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGTK  
IPGNWQIKIRPTAAIATGSSRNKPLANSPLCPGGCSCDHI PGSGLKMNCCNNRVSSSLADLKP  
KLSNVQELFRLDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRLWLYMDSNY  
LDTLSREKFAGLQNLEYLNVYNAIQILIPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL  
SKLSLHNHYFMYLPVAGVLDQLTSIIQIDLHGPNWECSCSTIVPFKQWAERLGSEVLMSDLKC  
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL  
VPGLLLVFVTSFTVVGMLVFILRNKRKRKRDRANDSSASEINSLQTVCDSSYWHNGFPYNADG  
AHRVYDCGSHSLSD

### Signal sequence:

amino acids 1-15

### Transmembrane domain:

amino acids 618-638

### N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

### Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

### N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

### Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

## FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCTCGACCCAGAATAACTCAGGGC  
TGCACCGGGCCTGGCAGCGCTCCGCACACATTTCTGTGCGCGCCTAAGGGAACTGTTGGC  
CGCTGGGCCCGCGGGGGGATTCTTGGCAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGG  
AAGGGAGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC  
AGCTCTGCGTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCAGGGCCTCAG  
AGAATGAGGCGCGGCTTCGCCCTGTGCTCTCTGCGAGGCGCTCTGGCCCGGGCCGGGCGG  
CGGCGAACACCCCACTGCCGACCGTGCTGGCTGCTCGGCCCTCGGGGGCCTGCTACAGCCTGC  
ACCACGCTACCATGAAGCGGCGAGCGCGCGAGGAGGCTGCATCTCTGCGAGGTGGGGCGCTC  
AGCACCGTGCGTGCGGGCGCCGAGCTGCGCGCTGTGCTGCGGCTCCTGCGGGCAGGCGCCAGG  
GCCCGGAGGGGGCTCCAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCACCACT  
GCACCTTGGAGAACGAGCCTTTGCGGGGTTTCTCTGGCTGTCTCCGACCCCGGCGGTCTC  
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCTCTGCACCGCGCGGAGATGCGC  
GGTACTCCAGGCCACCGGTGGGGTGCAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC  
GCGCCAACGGCTACCTGTGCAAGTACCAGTTGAGGTCTTGTGTCTGCGCGCGCGCCCGGG  
GCGGCTCTAATTGAGCTATCGCGCGCCCTTCCAGCTGCACAGCGCGCTCTGGACTTCAG  
TCCACTGGGACCGAGGTGAGTGCCTCTGCGGGGACAGCTCCCGATCTCAGTTACTTGCA  
TCGCGGACGAAATCGCGCTCGCTGGGACAACTCTCGGGCGATGTTGTGTCTCCCTGCCCC  
GGGAGGTACCTCCGTGCTGGCAAAATGCGCAGAGCTCCCTAAGTGCCTAGACGACTTGGGAGG  
CTTTGCTTGCAGATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCGCTCTTGTGTGACCA  
GTGGGGAAGGACAGCCGACCCTTGGGGGACCGGGGTGCCACCAGGCGCCCGCGGCCACT  
GCAACCGACCCCGTGCCGAGAGAACATGGCCAATCAGGGTGCAGGAGAAGCTGGGAGAGAC  
ACCACTTGTCCCTGAACAAGACAATTGAGTAACATCTATTCTGAGATTCTCGATGGGGAT  
CACAGAGCAGATGCTACCCCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC  
CCATCAGGGAGCGTGATTTCCAAGTTTAATTTCTACGACTTCTCTGCCACTCTCAGGCTTT  
CGACTCTCTCTGCGCGTGGTCTTCATATTTGTGAGCAGCAGTAGTAGTGTGTGGTGATCT  
TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTCA CGAAAGCCCTCTTCCCAGCCA  
AGGAAGGAGTCTATGGGGCCCGCGGGCCTGGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTC  
CAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCCGGGACTGTGATCTGCGGGACAGAG  
CAGAGGGTGCCCTGCTGCGCGAGTCCCCTCTTGCTCTAGTGATGCATAGGAAACAGGGGA  
CATGGGCACCTCTGTGAACAGTTTTCACCTTTGATGAAACGGGGAACCAAGAGGAACTTAC  
TTGTGTAACTGACAATTTCTGCAGAAATCCCCCTTCTCTAAATTCCTTTACTCCACTGAG  
GAGCTAAATCAGAACTGCACACTCTTCCCTGATGATAGAGGAAGTGGAAGTGCCCTTAGGA  
TGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTCGGAGAA  
TTTGAGAGAAGTGATTGAACCTTTCAAGACATTGGAAACAAATAGAACACATAATAATTACA  
TTAAAAAATAATTTCTACCAAATAAGGAAAGTGTCTATGTTGTTCCAGGCTAGGAGTAT  
ATTGGTTGCAATCCCAGGGAAAAAATAAAAAATAAAATTAAGGATTGTTGAT

## **FIGURE 36**

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS  
TVRAGAE LRAVLALLRAGPGPGGGSKDLLFWVALEERRRSHCTLENEPLRGFSWLSSDPGGLE  
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPGA  
ASNL SYRAPFQLHSAALDFSPGTEVSALCRGQLPISVTCIAD EIGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTS GEGQPTLGGTGVPTRRPPATA  
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTSSATPQAFDSSSAVVFI FVSTAVVVLVILTM TVLGLVKLCFHESPSSQPR  
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDR AEGALLAESPLGSSDA

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 399-418

### **N-glycosylation site.**

amino acids 189-193, 381-385

### **Glycosaminoglycan attachment site.**

amino acids 289-293

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

### **Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

### **N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

## FIGURE 37

CGGACGCGTGGGATTACAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG  
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAAGTGCCCTCCGCCCTGCCGGCCGCGTATC  
CCCCGGCTACCTGGGCCGCCCGCGCGCGTGCAGCGGTGAGAGGGAGCGCGCGGGCAGCCGA  
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGCGTGTGAGCGCGGTGGGTGCGGA  
GGGGCGTGTGTGCCGGCGCGCGCCGTGGGGTGCAAAACCCGAGCGTCTACGCTGCC**ATGA**  
GGGGCGCGAACGCCTGGGCCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG  
CAGCAGTCCCCAGAGAGACCTGTTTTCACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT  
TATTGGCAGTGAAGGTTTTCTGGAGTGTACCCTCCAAATAGCAAATGTACTTGGAAAAATCA  
CAGTTCGCCGAAGGAAAAAGTAGTCGTTCTCAATTTCCGATTTCATAGACCTCGAGAGTGACAAC  
CTGTGCCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTGGCCG  
CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA  
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAC  
CCCCAACTGGCCAGACCGGGATTACCTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCCC  
CAAAGAATCAGCTTATAGAATTAAGTTTGAGAAGTTTGATGTGGAGCGAGATAACTACTGC  
CGATATGATTATGTGGCTGTGTTAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA  
GTATTGTGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTCTTATTTCAGT  
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTTCAGGCCAAAA  
AAACTGCCTACAACCTACAGAACAGCCTGTCAACCCACACATTCCCTGTAACCAACGGGTTTAAA  
ACCCACCGTGGCCCTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT  
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAACCATCACTCGCGATGGGAGTTTG  
CACGCCACAGTCTCGATCATCAACATCTACAAGAGGGAAATTTGGCGATTTCAGCAGGCGGG  
CAAGAACATGAGTGCCAGGCTGACTGTGCTCTGCAAGCAGTGCCCTCTCCTCAGAAGAGGTC  
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAAACAGC  
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAATAAGCAATG  
**TTAA**CAGTGAACGTGTGCCATTTAAGCTGTATTCTGCCATTGCCCTTTGAAAGATCTATGTTCT  
TCTCAGTAGAAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG  
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCCTCCGAGATAGCTGAGGGAGATTCTT  
TGCCCTGCTGCAGAGGAGCAGCTATCTGATTGGAACCTGCCGACTTAGTGCGGTGATAGGA  
AGCTAAAAGTGTCAAGCGTTGACAGCTTGAAGCGTTTTATTATACATCTCTGTAAAAGGAT  
ATTTTGAATTTAGTGTGTGAAGATGTCAAAAAAAGATTTTAGAAGTGCAATATTTATAGT  
GTTATTGTTTCCACTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGGCTTTCTA  
AATCAATGCTTAATAAAATATTTTTAAAGGAAAAAAAAAAAA

## **FIGURE 38**

MRGANAWAPLCLLLAAATQLSRQQSPERFVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK  
ITVPEGKVVLNFRFIDLESNDLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI  
QFLSDLSLTADGFIGHYIFRPKILPTTTEQPVTTTFPVTTGLKPTVALCQQKCRRTGTLEG  
YCSSDFVLGTVITTTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLR  
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

### **Signal sequence:**

amino acids 1-23

### **N-glycosylation site.**

amino acids 355-359

### **Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

### **Tyrosine kinase phosphorylation site.**

amino acids 199-208

### **N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

### **Cell attachment sequence.**

amino acids 149-152

## FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTCGCTTCTT  
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCCAGGACCTATCTGG  
CTCCAGCCCTCTCCACCTCCCAGTCTTCTCCCCGCTCAGCCCCATCCGTGTATACCTG  
CCGGGGACTGGTTGACAGCTTTAAACAAGGCCCTGGAGAGAACCATCCGGGACAACCTTTGGAG  
GTGGAAACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCTG  
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCTGTGGAGCT  
GAGTGAGGAGCTGTGGAGAGCTGGTGGTTTACAAAGCAGCAGGAGGCCCGGACCTCTTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCCGAGGCACCTTCGGGCCCTCTGTC  
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG  
GACACGAGGGGGCAGCGGGCAGTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC  
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT  
TTTGGCCCTGTGCCCCGATGCTCAGGACCTGAGGAATCAAAGTGTTCGCAATGCAAGAAGGG  
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT  
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG  
GCCTGCCTAGGCTGCATGGGGGAGGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA  
ACAAGCAGTGTGAAAAACCCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG  
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA  
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG  
ACTGGCTACTGGTTGTGTCAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA  
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCCAGAGCTTGGGCTGCCC  
TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTGTAGAGTGGGGTAAGCACCCTACCTG  
CCTTACAGAGCAGCCCAGGTATCCAGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC  
CCTGAAGGTGGATACCATGAGCTTTCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGA  
ATTTCAAAGTTTTCCTTAATGGTGGCTGCTAGAGCTTTGGCCCTGTCTAGGATTAGGTG  
GTCTCTCAGAGGGTGGGGCCATCACAGCTCCCTCCTGCCAGTGCATGTGCCAGTTCTGT  
TCTGTGTTTACCACATCCCCACACCCATTGCCACTTATTATTATCTCAGGAAATAAAGA  
AAGTCTTGGAAAGTTAAAAA

## **FIGURE 40**

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER  
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ  
QEAPDLFWLCCSDSLKLCPPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDQAG  
YGGACGQCGLGYFEARNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE  
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE  
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLLQQMFFG  
IITCALATLAAKGDVFTAIFFIGAVAAMTGYWLSERSDRVLEGFIKGR

### **Signal sequence:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 372-395

### **N-glycosylation site.**

amino acids 79-83, 205-209

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

### **Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

### **N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

### **EGF-like domain cysteine pattern signature.**

amino acids 181-193



## FIGURE 41

TGAGACCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA  
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACCTCTGGGTGTTGCCCTGGCCAGCCCCGGG  
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGT  
GCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGGCCAGT  
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGGAAAGAGGTTCAGCCAGAGC  
TTCGAGAGAGGTGGCCGGCAGGTTCTTGGCGTTGGAGGCCAGCACACCTGCTGGTGTTCGG  
CATGGAGCAGCGGCTGCCGCCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTTCCAGG  
AGCCCGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCGCGCAGCGCCCGGGCC  
CGGGTGACCGTCGAGTGGCTGCCGCTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA  
CTCCAGGCTGGTGTCCGTCACGAGAGCGGCTGGAAGGCCCTTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGTACAGGTGTCGGTGCAGAGG  
GAGCATCTGGGCCCCGTGGCGTCCGGCGCCCAAGCTGGTCCGCTTTGCCCTCGCAGGGGGC  
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCTGGACCTTGGGGACTATGGAG  
CTCAGGGCGACTGTGACCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG  
ATGTACATTGACCTGCAGGGGATGAAGTGGGCGGAGAACTGGGTGCTGGAGCCCCGGGCTT  
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTTCAAGTGGC  
CGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA  
GTGCAGCTGTCCCTCGGATGGTGGCTCGTGCCAAGGAGGCTCCAGCCATTAGGCGCCCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTCTTCTGAAGTGTTCGAGGGTACCAGGAGAGCTG  
GCGATGACTGAAGTCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT  
CCTCTGACAAGTTACCTCACCTAATTTTGTCTTCTCAGGAATGAGAATCTTTGGCCACTGGA  
GAGCCCTTGCTCAGTTTTCTCTATTCTATTATTCACTGCACCTATATTCTAAGCACTTACAT  
GTGGAGATACTGTAACTGAGGGCAGAAAGCCCCANTGTGTCATTGTTTACTTGTCTGTGCAC  
TGGATCTGGGCTAAAGTCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT  
TGTGCATCCCCAATCCAGATAATAAAGACTTTGTAAAAATGAATAAAACATTTTATTCTT  
AAAA

## **FIGURE 42**

MQPLWLCWALNVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV  
ALLQRSHGDRSRGKRFSQSFRVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP  
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSGNRTSLIDSRLVSVHESGWKAFDVT EAVNF  
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLDYGAQ  
GDCDPEAPMTETGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCTCRQPPEALAFKWP  
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLEPNMRVQKCSASD GALVPRRLQP

### **Signal sequence:**

amino acids 1-18

### **N-glycosylation site.**

amino acids 158-162

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

### **N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

### **Amidation site.**

amino acids 74-78

### **TGF-beta family signature.**

amino acids 282-298

## FIGURE 43

GTCTGTTCCAGGAGTCCCTTCGGCGGCTGTTGTGTGTCAGTGCCCTGATCGCGATGGGACAAA  
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGTCTCCCTGG  
CATTTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT  
GTGAAGTTGTCTGTGCCTACTCGGCTTTTCTTCTCCCCGTGTGGAGTGAAGTTTGACCA  
AGGAGACACCACCAGACTCGTTTGTCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG  
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGTTCATCGT  
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCTCTGCCACCATTGGGAACCGGG  
CAGTGTCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACA CCTGGTTCAAAGAT  
GGGATAGTGATGCCACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCCT  
GAATCCCAACAACAGGAGAGCTGGTCTTTGATCCCTGTGAGCCTCTGATACTGGAGAATACA  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT  
GTGGAGCGGAATGTGGGGGTCACTCGTGGCAGCCGTCCTTGTAAACCTGATTCTCCTGGGAAT  
CTTGTTTTTGGGCATCTGGTTTGGCTATAGCCGAGGCCACTTTGACAGAAACAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCTCGGTGTGAGCCTGGTTCGGCTCACCGCCTATCATCTGCATTGGCCTTACT  
CAGGTGCTACCGGACTCTGGCCCCGTGATGTCTGTAGTTTACAGGATGCCCTTATTGTCTTC  
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTGAGCTATGTCCCC  
ATCCTCCTTCATGCCCTCCCTCCCTTCTCCTACCACTGCTGAGTGGCCTGGAACCTTGTTTAA  
GTGTTTATTTCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGCAAAAATGGCGGGGTCGAGGAATCTGCACTCAACTGCCACCTGGC  
TGGCAGGGATCTTTGAATAGGTATCTTGAGCCTGGTTCTGGGCTCTTCTCTGTCTTCCATGGGAAGT  
TGATGACACTGGGGTCTTCCATCTCTGGGGCCCCACTCTCTTCTGTCTTCCATGGGAAGT  
CCACTGGGATCCCTCTGCCCTGTCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT  
GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTTCAGAGAACTTGAAGCCAAAAG  
GATTTAAACCGCTGCTCTAAAGAAAAGAAAATCGGAGGCTGGGCGCAGTGGCTCACGCCTG  
TAATCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGCGGAGTTGCGGATCAGCCTGACCA  
ACATGGAGAAACCTTCTGGAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPFVKLS CAYSGFSSPRVEW  
KFDQGDTRLVCYNNKITASYEDRVTFLEPTGITFKSVTR EDTGTYYTCMVSEEGNSYGEVKV  
KLIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS  
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGT PMTSNAVRMEAVERNVGVIVA AVLVTLI  
LLGILVFGIWFAYS SRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

### **Signal sequence:**

amino acids 1-27

### **Transmembrane domain:**

amino acids 238-255

### **N-glycosylation site.**

amino acids 185-189

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

### **Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

### **N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

## FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCA**ATG**AGCGGCGGTTGGATGGCGCAGGTTGGA  
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGA**CTAGGCCT**  
GGAGGCCCGCCGAGCCCGCTTTCCACCCCGACCTCTGCCAGGCCGAGGCCCCAGCTCAG  
GCTCGTGCCACCCACCAAGTTCCAGTGCCCGACCA**GTGGCTTATGCGTGCCCTCACCTGG**  
CGCTGCGACAGGGACTTGGA**CTGCAGCGATGGCAGCGATGAGGAGAGTG**CAGGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCACCGCC**CTGGCTCCCTGCCCCTGCA**CCGGCGTCA  
GTGACTGCTCTGGGGGA**ACTGACAAGAACTGCGCAA**CTGCAGCCGCTGGCCTGCCTAGCA  
GGCGAGCTCCCGTTGCACGCTGAGCGATGACTGCAT**TCCACTCACGTGGCGCTGC**GACGGCCA  
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAA**CCAATGAGATCCTCCCGAAG**  
GGGATGCCACAACCATGGGGCCCCCTGTGAC**CTGGAGAGTGTCACTCTCTCAGGAATGCC**  
ACAACCATGGGGCCCCCTGTGAC**CTGGAGAGTGTCCCTCTGT**CGGGAATGCCACATCCTC  
CTCTGCCGAGACCA**GTCTGGAAGCCCACTGCC**TATGGGGTTATTGCAGCTGCTGCGGTGC  
TCAGTGCAAGCCTGGTCACCGCCAC**CTCCTTCTTGTCTGGCTCCGAGCCAGGAGCGC**  
CTCCGCCCACTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTCAGAACAGAA**AGAC**  
CTCGCTGCCCT**TGA**GGACAAGCACTTGCCACCACC**GTCACTCAGCCCTGGGCGTAGCCGACA**  
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAA**GTGGCCCTGGAGATTGAGGGTCCC**  
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAAC**TGCCACAGCCAGA**ACTGAG  
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG  
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

## **FIGURE 46**

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCDRDLDCSDGSDEEECRIEPTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL  
RNC SRLACLAGE LRCTLSDDCIPLTWRC DGH PDCPDSSDELGCCTNEILPEGDATTMGPPVT  
LESVTS LR NAT TMGPVVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL  
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTS LP

### **Signal sequence:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 230-246

### **N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

### **Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

### **N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

### **Leucine zipper pattern.**

amino acids 17-39

## FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGCGCGGCAGCAGAGGTCGCGCACAGATGCGG  
GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA  
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG  
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG  
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT  
CGATGACCTTCAAGTGTGTGTGACCCCGGCATTCCCAGAAATGGCTTCAGGACCCCCAGCG  
GAGGGGTTTCTTTGAAGGCTCTGTAGCCCGATTTCAGTGCCTAAGCGGATTCAAGCTGAAG  
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAAATGGAACCTTAGGCTGGATCCCAAGTGA  
TAATTCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTGATA  
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTGCATGAAGGATTCAAGATCCGG  
TACCCCGACCTACACAATATGGTTTCATTATGTGCGGATGATGGAACGTGGAATAATCTGCC  
CATCTGTCAAGGCTGCCTGAGACCTTAGCCTCTTCTAATGGCTATGTAACATCTCTGAGC  
TCCAGACCTCCTTCCCGTGGGACTGTGATCTCCTATCGCTGCTTCCCGGATTTAAACTT  
GATGGGTCTGCGTATCTTGAGTGTCTACAAAACCTTATCTGGTCTGCCAGCCACCCCGGTG  
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGCT  
GCCACCCGCGGCTTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTTACTGCGATCCT  
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCTTC  
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCTCTCTGA  
CCACGTGGAAGATTGTGGCGTTACGGGCAACCAGTGTGCTGCTGCTGCTGCTGCTGCTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCCACTTCCCCCAGGGGGCTTCCCCGGAG  
TTCCAGCAGTGACCCTGACTTTGTGGTGGTAGACGGCGTGCCGTCATGCTCCCGTCTCTATG  
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCGGGTACATGGCCTCTGTGGGCCAG  
GGCTGCCCTTACCCGTGGACGACAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA  
CACAGGCCAGGGGAGTCAGAACTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA  
GTCTGTATTACCTCCAGGTGCCAAGAGAGCACCACCTGCTTCGGACAACCTGACATA  
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACAGCCAGGCATCCATCATGCCACTGGGT  
GTTGTTCTTAAGAACTGATTGATTAAAAAATTTCCCAAAGTGTCTGAAGTGTCTCTTCAA  
ATACATGTGTGATCTGTGGAGTTGATTCTTCTTCTTCTGTTTGTAGACAATGTAAACAA  
AGCTCTGATCCTTAAATGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC  
CTGTTTCTTCTTGACACAGACTGATTAAAAATTTAAAGNAAAAA

## FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI  
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFFGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLP  
PMVSHGDFVCHFRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTTWKIVAFTATSLLVLLVILARMFQTKFAHFPPRGPPRSSSDPFDVVVD  
GVPVMLPSYDEAVSGLSALGPGYMASVGGCPLPVDQSPPAYPGSGD TDTGPGESETCDS  
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVLFRLN

### Signal sequence:

amino acids 1-41

### Transmembrane domain:

amino acids 325-344

### N-glycosylation site.

amino acids 104-108, 134-138, 192-196

### Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

### N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

### Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405



## FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTCCGGTCCGTCCGGTGGCCTAGAGA  
TGCTGCTGCCGCGGTTGCAGTTGTGCGGCACGCCTCTGCCCGCCAGCCCGCTCCACCGCCGT  
AGCGCCCGAGTGTGCGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGGAACCGCGCTACAGG  
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGTCTCGGGCCGCGACGGGTGCGCTGTGAGTGCC  
TCGGATTGGAACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCTTGTTA  
TAAAGTCATTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA  
AAGTTCATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA  
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT  
CACAAITTAGGAAC TGGTATGTGGATGAGCCGTCTGCGGCAGCGAGGTCTGCGTGGTCATG  
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA  
CCGGTGCAACATGAAGAACAAITTCATTTGCAAAATATTCTGATGAGAAACCAGCAGTTCCTT  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCAGAAGAAACACAG  
GAAGAAGATGCCAAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCCTACAT  
CCTAATCCCCAGCATTCCCCTTCTCCTCCTCTTGTGTCACCCACAGTTGTATGTTGGGTTT  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCTAGCACAAAGAAGCAACACACCATC  
TGGCCCTCTCCTCACCGGAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTCAITCCGAGTGTGTT  
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA  
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTGTGACCAATGACATTTATGA  
GTTCTCCCCAGACCAATGGGGAGGAGTAAGGAGTCTGGATGGGTGAAAATGAAATATATG  
GTTATTAGGACATATAAAAACTGAAACTGACAACAATGGAAGAAAGAAATGATAAGCAAAATC  
CTCTTATTTTCTATAAGGAAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCTGT  
GGATGAGCATGTGGTCCCCACGACCTCTGTGGACCCCCACGTTTGGCTGTATCCTTTAT  
CCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCAGGTCTGGCACATAGTA  
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG  
GCAGTGATAAAGATGGGCTGTGGAGCTTGGAAGAACACCTCTGTTTTCTTGTCTATACAG  
CAGCATATATTATCATAAGACAGAAAAATCCGAATCTTTTCAAAGCCCATATGTTAGCAGAG  
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTTCAAAGAATAAAATCAAATAAAGA  
GCAGGAAAAAAA

## **FIGURE 50**

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGTQRPCYKVIYFHDTSRRL  
NFEEAKEACRRDGGQLVSI ESEDEQKLEKFIENLLPSDGD FWIGLRREEKQSNSTACQDL  
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY  
SDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAAALNLAYILI PSIPLLLLLV  
VTTVVCVWVICRKRKREQDPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL  
KNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTILVSVESGFVTNDIYEFSPDQMGRSKES  
GWVENEIYGY

### **Signal sequence:**

amino acids 1-21

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 117-121, 312-316

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

### **Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

### **N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGCGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT  
GTTTGCCCTCCTGCAGCCTCAACCCGAGGGCAGCGAGGGCCTACCACATGATCACTGGTGT  
GTTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCTGACCTCGCTGGCGTACTGCTGCACC  
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTGCACCGCAGC  
CTGCTGAAGTTGAAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC  
GCTCCCGCTGGAGGAGCAGGTAGAGTGAACCCCCAGCTATTAGAGGTCCCACCCCAAACCTC  
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT  
CAATACCATGAGACCACCTGAAGGGGGGCATGTTTGTGGGCAGCTGACCAAGGTGGGCAT  
GCAGCAAATGTTTGCCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCTTTTC  
TTTACCACCACTTCAACCCACAGGAGGTCTTTATTTCGTTCCACTAACATTTTTCGGAATCTG  
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCAGTGTGAGAAAGAAGGACCCATCATCAT  
CCACACTGATGAAGCAGATTCAGAAGTCTTGTATCCCACTACCAAGCTGCTGGAGCCCTGA  
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTG  
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGAAGTCTTTCATCCTCCT  
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTG  
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGTGTATCTCTATGCGGCTCATGATG  
TGACCTTCATACCGCTCTTAATGACCTGGGGATTTTGTGACCACAAATGGCCACCGTTTGCT  
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCGAGCTCTA  
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT  
TCTTGAATGCCATGTGAGTTTATACCTTAAGCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAATGAAGAGTAACTGATTTATAAAGCAGGATGTGTTGATT  
TTAAATAAAGTGCCCTTTATACAATG

## **FIGURE 52**

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLMVQVVRHGAR  
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL  
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE  
GPIIIHTDEADSEVLYPNYQSCWSLRQTRGRRQTASLQPGISEDLKVKVKDRMGIDSSDKVD  
FFILLDNVAEQAHNLPSCPMCLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLLHILES  
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW  
FVQLYYHGKEQVPRGCPDGLCPIDMFLNAMS VYTLSP EKYHALCSQTQVMEVGNEE

**Signal sequence:**

amino acids 1-23

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 218-222

**Casein kinase II phosphorylation site.**

amino acids 87-91, 104-108, 320-324

**Tyrosine kinase phosphorylation site.**

amino acids 280-288

**N-myristoylation site.**

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

**Amidation site.**

amino acids 216-220

**Leucine zipper pattern.**

amino acids 10-32

**Histidine acid phosphatases phosphohistidine signature.**

amino acids 50-65

## FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGTGCTTGGGGACCTCCTTCTAGCCT  
TAAATTTTCAGTCTCATCACCTTCACCTGCCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTTGCACCAGACCTGGATTCTTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG  
ACGGCTGGGACATTAAAGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG  
ATTGTTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCCA  
GTCCCAGAGGGTGTGAGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA  
GCACCAGAACCAGTGGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCGCAAAGGTGG  
TGTGCCGGCAGCTGGGATGTGGGAGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC  
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCTAGCTCAGGACGAGAAGCAACCTTCA  
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTG  
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG  
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTCTGTGATGACAACCTGGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA  
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTGCTTGCTCAGGGGAGGAG  
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA  
TGTGGCTGTCTGCTCAGTGTTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA  
GAAAAACAGAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT  
TCTTCTGCCCTTGAGCTGGGACTTATACTTGGTGCCCTTGATTCTCAGGCCTTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTTTCTCAGGCCATCAGACATAGTTTGGAACTACATCA  
CCACCTTTCCTATGTCTCCACATTGCACACAGCAGATTCACAGCCTCCATAATTGTGTGTAT  
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACATA  
CACCATTGTCTGTTTCTCTGAAGAACTCTGACAAAAACAGATTTTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTTTAAAGATAAATTTCTGAATTGGTTATGGGGTTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTTCTGGTAACTTTATTTACAATAATAAAGATAGCAC  
TATGTGTTCAA

## **FIGURE 54**

MALLFSLILAICTRPGFLASPSGVRLVGGGLHRCCEGRVEVEQKGQWGTVCDDGWDIKDVAVL  
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEVEYDCSHDEAGASC  
ENPESFSFVPEGVRLADGPGHCKGRVEVKHQNQWYTVCTGWSLRAAKVVCRLGCGRAVL  
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPGWGKNTCNHDEDTWVECEDPFDLRLVG  
GDNLCSGRLEVLHKGVWGSVCCDNWGEKEDQVVKQLGCGKSLSPSFRDRKCYGPGVGRIWL  
DNVRCSGEEQSLEQCQHRFGWGFHDCTHQEDVAVICSV

### **Signal sequence:**

amino acids 1-15

### **Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

### **N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

### **Amidation site.**

amino acids 196-200

### **Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

## FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCGGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGCGCTGCTGGG  
CGTCTTCGGCTCTTCCGCTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCGGAATGCTG  
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT  
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAAGACTCATCAGAGA  
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC  
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC  
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA  
TGTGGACAAGAGGGTCATGGAGACAACTACTTTGGCCAGTTGCTCTAACGAAAGCACTCC  
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA  
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC  
ACCACCACAGCCCAGGGCCGAAGCCTGTGGAGGTGGCCAGGATGTTCTTGCTGCTGTGGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA  
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC  
AAGAACTCCTTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC  
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTTGTCTCACAAGTGGG  
AAAGACTGAAGAAACACATCTCGTGAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA  
AGCTTCTTCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTAACT  
AAAACTAGAAATAACATCTCAAACAGTAAAAAAAAAAAAAAGGGCGGCCGCACTTAG  
AGTCGACCTGCAGAAGCTTGGCCGCATGGCCCAACTTGTTTATTGCAGCTTATAATGTTAC

## **FIGURE 56**

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA  
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL  
VNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQ GKMSI  
PFRSAYAASKHATQAFDCLRAEMEQYBIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT  
AQGRSPVEVAQDVLAAVGGKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

### **Signal sequence:**

amino acids 1-21

### **Transmembrane domain:**

amino acids 104-120, 278-292

### **N-glycosylation site.**

amino acids 228-232

### **Glycosaminoglycan attachment site.**

amino acids 47-51

### **Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

### **Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

### **N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

### **Amidation site.**

amino acids 265-269

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17



## FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA  
AAAAAAAAACACACCAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC  
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCTTCGTGAAGCTTTTTATCTTAA  
GAGGAGAAAATCAGTCACCGGCGAAATCGTCTGATTACAGGAGCTGGGCATGGAATTGGGA  
GACTGACTGTCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG  
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTTGT  
GGTAGACTGCGACAACCGAGAAGATATTTACAGCTCTGCAAGAAGGTGAAGGCAGAAATTG  
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA  
CAAGATCCTCAGATTGAAAAGACTTTTGAAAGTTAATGTACTTGCAATTTCTGGACTACAAA  
GGCATTTCCTCCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG  
CTGGACATGTCTCGGTCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA  
TTTCATAAACTTTGACAGATGAACTGGCTGCCTTACAAATACTGGAGTCAAAACAACATG  
TCTGTGTCCCTAATTTGCTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA  
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCAATGGGATTCTGACTGAGCAGAAGATG  
ATTTTTATTCCATCTTCTATAGCTTTTAAACAACATTGGAAAGGATCCTTCCTGAGCGTTT  
CCTGGCAGTTTAAACGAAAAATCAGTGTAAAGTTTGATGCAAGTTATTGGATATAAATGA  
AAGCGCAATAGGCACCTAGTTTTCTGAAAACAGTTTACCAGGTTTAGGTTGATGTCTCTA  
ATAGTGCCAGAATTTAATGTTTGAACCTCTGTTTTTCTAATTATCCCCATTTCTTCAATA  
TCATTTTGGAGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT  
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA  
CCAAAATGACTTTATTAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA  
AATTTGTACCATAACCGTTTATTTAACATATATTTTATTTTGATGCACTTAAATTTTGT  
ATAATTTGTGTTTCTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA  
TGAAGGACTATATCTAGTGGTATTTTCAATGAATATCATGAACCTCTCAATGGGTAGGTTTC  
ATCCTACCCATTGCCACTCTGTTTCTGAGAGATACCTCACATTCGAATGCCAAACATTTCT  
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG  
GAGAAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 58**

MKFLLDILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK  
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAEIGDVSILVNNAGVV  
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTASAAGHVSVPFLAYC  
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH  
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

### **Signal sequence:**

amino acids 1-19

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-34, 283-287

### **Casein kinase II phosphorylation site.**

amino acids 52-56, 95-99, 198-202, 267-271

### **N-myristoylation site.**

amino acids 43-49, 72-78, 122-128, 210-216

## FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTGCGACTAGTTCTAGATCGCGAGCGGCCGCCCGCGGCTC  
AGGGAGGAGCACCGACTGCGCCGCACCTTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG  
TTTCGCTGGTCTGTGATGCTGGCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT  
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC  
TGGGAAGATCCAAAAAGGAAGAGAATTGAGTTTGGTCCGCCCTTCCAGGACTGAACATGA  
AGAGTTATGCGCGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTCTGGTTC  
TTCCACAGTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG  
AGGTTCAATCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTACAAAGTAACATGA  
CCTTGGCTGACAGAGACTTCCCTGGACCAACAACGCTCTCCATGCTTTACATTGACAATCCA  
GTGGGCACAGGCTTCAAGTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT  
AGCACGGGATTTATACAGTGCCTAATTCAAGTTTTCAGATATTTCTGAATATAAAAAATA  
ATGACTTTTATGTCACTGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC  
ATCCATTCCCTCAACCCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA  
TGGATATTTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCT  
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC  
AGGAAGCAGAAGCTGGTTTGAGGCCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC  
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAAATTTTGGCGGT  
GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTGTCACTCCAGAGGTGAGACAA  
GCCATCCACGTGGGGAAATCAGACTTTTAATGATGGAACATATAGTTGAAAAGTACTTGCAGAA  
AGATACAGTACAGTCAAGTAAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA  
TCTACAATGGCCAACCTGGACATCATCGTGGCAGCTGCCCTGCACAGAGCGCTCTTGATGGGC  
ATGGACTGGAAAAGGATCCAGGAATACAAGAAGGCAGAAAAAAGTTTGGAAAGATCTTTAA  
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTC  
GAGGTGGAGGACATATTTTACCCTATGACCCAGCCCTCTGAGAGCTTTTGACATGATTAATCGA  
TTCATTTATGGAAAAGGATGGGATCCTTATGTTGGATAAACTACCTTCCCAAAAGAGAACAT  
CAGAGGTTTTCATTGCTGAAAAGAAAATCGTAAAAACAGAAAAATGTCATAGGAATAAAAAA  
TTATCTTTTATATCTGCAAGATTTTTCATCAATAAAAAATTATCTCTGAAACAAGTGAGC  
TTTTGTTTTTGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA  
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAAGATGTATAAATGA  
AATTTTAGGGCTTGAATAGGAAGTTTAAATTTCTTCTAAGAGTAAGTGAAAAGTGCAGTTG  
TAACAAACAAAGCTGTAACATCTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT  
GTTTGGAAATATTATGGATAAGAATAGCTCAATTATCCCAATAAATGGATGAAGCTATAA  
TAGTTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACCAAGAAATTTCTTTGAAATA  
AAAATATTATATATAAAGTAAAAA

## **FIGURE 60**

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPPKGDGSQLFLTPYIEAGKIQKGRELSL  
VGPFPGLNMKSYAGFLT VNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPVYVTSNMTLRDRDFPWTITLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQQ  
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLSLNPVREVKINLNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFIELDKLLDGLTSDPSYFQNVGTG  
CSNYYNFLRCTEPEDQLYYVVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT  
EIMNNYKVLIIYNGQLDIIIVAAALTERSLMGMDWKGSQEYKKAEEKVWKIKFSDSEVAGYIRO  
AGDFHQVVIIRGGGHILPYDQPLRAFDMINRFIYGKGNWDPYVG

### **Signal sequence:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

### **Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

### **Tyrosine kinase phosphorylation site.**

amino acids 423-432

### **N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

### **Serine carboxypeptidases, serine active site.**

amino acids 200-208

### **Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

## FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTGGCTACAACAT  
TTTTCCCTTTCTTAACAAGTTCTAACAGCTGTCTAACAGCTAGTGATCAGGGGTTCTTCTT  
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCAGCTCTCACTCAGGGTGACCAAGTCCCTTG  
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG  
TCTAAAAATAGGAAGGAATTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC  
CTGGGGGAGGGCTGCCTAACAAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT  
AAGACGTGCCGATAGGATAGGGAAGACTGGGTTAGTCTTAATATCAAATTGACTGGCTGGG  
TGAACTTCAACAGCCTTTTAACTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA  
TAGAGATGCTTTGTAAAAATAAAATTTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATTCCCTGAACATTCCTAAGAGGGAGAAAGTATGTTAAAAATA  
GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGAGCCCTGGGTC  
AGGCCAGCCTCTTTGCTCTCTCCCGAAATTATTTTGGTCTGACCACCTCTGCCTTGTGTTTT  
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACAGGAGCCGTCT  
CCTCACCGCCGCCCTCTCAGCATGGAAACAGAGGCAGCCCTGGCCCGGGCCCTGGAGGTGG  
ACAGCCGCTCTGTGGTCTGTCTCAGTGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC  
ATGCTCAGTTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACCTTGACCGT  
CCACCAAGGGACGGGGCCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA  
ACCTGACCATCCAGTGGCTCATAAAGACAGGGCCAGAAGAGGACAACAGTCTCGTTACCCG  
CCCCCTCATCGTGACGCCCTGCAGCGAAGTGCTCACCTCACCACAATGTCAACAAGCTGCT  
CATCATTGACTACTCTGAGAACCGCTGTCTGGCCTGTGGGAGCCTCTACCAGGGGTCTGCA  
AGCTGTGCGGCTGGATGACCTCTTCATCTTGGTGGAGCCATCCACAGAAGGAGCACTAC  
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTGATTGTGCCTCTGAGGTTGAGGA  
TGGAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCTGTCCA  
GCCGAAGCTGCCCGAGACCCTGAGTCTCAGCCATGCTCGACTATGAGCTACACAGCGAT  
TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCACTTTGACAT  
CTTCTACATCTACGGCTTTGTCTAGTGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA  
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCAGCATCGTGC  
CTCTGCAAGGATGACCCCAAGTTCCACTCATACTGTCTCTGCCCTTCGGCTGCACCCGGGC  
CGGGTGGGAATAACCGCTCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC  
AGGCCTTCAATATCACCAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAG  
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGTGCTTCCCTATCCGGGCCATCAACT  
GCAGATCAAGGAGCGCCTGCAGTCTTGCTACCAAGGCGAGGCAACCTCGGAGCTCAACTGGC  
TGCTGGGGAAGGACGTCCAGTGACGAAGGCGCCTGTCCCCATCGATGATAACTTCTGTGGA  
CTGGACATCAACCAGCCCTGGGAGGCTCAACTCAGTGGAGGGCCTGACCTGTACACCAC  
CAGAGGGACCGCATGACCTCTGTGGCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTG  
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAAGAGTCTATGAGTTCAGATGCTCCAATGCC  
ATTCACCTCTCAGCAACAGTCCCTCTTGGAAAGGTAGCTATTGGTGGAGATTAACTATAG  
GCAACTTTATTTTCTTGGGGAACAAAGGTGAAGTGGGAGGTAAAGAGGGTTAAATTTGTG  
ACTTAGCTTCTAGCTACTTCTCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA  
TTTCAATATTTCCCAACTTTAAGAAAAACTTTAAGAAGGTACATCTGCAAAAGCAA

## **FIGURE 62**

MGTLGQASLFAPPNGYFWSHSAALCFAESCEGQPGKVEQMSTHRSRLTLTAAPLSMEQRQPWP  
RALEVDSSRSVLLSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV  
YKLTGNLTIQVAHKTGPEEDNKSRYPLIVQPCSEVLTLTNVNKLLIIDYSENRLLAGCSL  
YQGVCKLLRLDDLFI LVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDQDY  
FTLSSRKLPDPRESSAMLDYELHSDVSSLIKIPSDTLALVSHFDIFYIYGASGGFVYFL  
TVQPETPEGVAINSAAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSLAQAFNITSQDDVLF AIFSKGQKYHHPPDDSAALCAFPPIRAINLQIKERLQSCYQEGN  
LELNWLLGKDVQCTKAPVIPDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG  
YSVVFVGTKSGKLKVRVYEFRCNSNAIHLLSKESLLEGSYWWRFNRYQLYFLGEQR

### **Signal sequence:**

amino acids 1-32

### **Transmembrane domain:**

amino acids 71-87

### **N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

### **Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

### **N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

## FIGURE 63

AGGCTCCCGCGCGCGGCTGAGTGCAGTGGAGTGGGAACCCGGTCCCCGCGCTTAGAGAACACGCGATGACCA  
 CGTGGAGCTCTCCGCGGAGGCCGCGCCGACGCTGGGACTCTGCTGCTGGTCTGCTTTGGGCTTCTGGTGCTCC  
 CGAGCTTGGACTGGAGCACCTGGTCTCTTGGCGCTCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA  
 ACTTTCAGTCTGAGGATTCACCTTCTGGATCTTCGGGGGCTCCATCCATCTATTTCCGTGTGCCACGGGAGTACT  
 GGAGGGACCCGCTGTCTGAAGATGAAGGCTGTGGCTTTGAACACCTCACACCTATGTTCCGTGGAACCTGCAATG  
 AGCCAGAAAGAGGCAAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCTTCTGCTGATGGCCGCAAGAGATCG  
 GGCTGTGGGTGATTCTTGGCTCCAGGCCCTACATCTGCAGTGAGATGGACCTCGGGGGCTTGCAGGCTGGCTAC  
 TCCAGAGCCCTGGCATGAGGCTGAGGACAACTTCAAGGGCTTCAACGAAAGCAGTGGACCTTTATTTTGAACAC  
 TGATGTCCAGGGTGGTGCCACTCCAGTACAAGCGTGGGGGACCTATCATTTGCCGTGAGGTGGAGAATGAATATG  
 GTTCTCTATAAAGACCCCGCATACATGCCCCACGTCGAAGAGGCACTGGAGGACCTGGGCACTTGTGGAACCTGC  
 TCTCGACTTTCAGACACCAAGGATGGGCTGAGCAAGGGGATTTGTCAGGGAGCTTCCGCCACCATCAACTTCCAGT  
 CAACACACGAGCTGCAGCTACTGACCACCTTTCTCTCAAGCTCCAGGGGACTCAGCCCAAGATGGTGATGGAGT  
 ACTGGACGGGGTGGTTTGACTCGTGGGGAGGCCCTCACATATCTTGGATTCTCTGAGGTTTTGAAAAACCGTGT  
 CTGCGATTGTGGACGCGGCTCTCCATCAACCTCTACATGTTCCAGGAGGACCAACTTTGGCTTCATGAATG  
 GAGCCATGCACTTCCATGACTACAAGTCAGATGTACCCAGCTATGACTATGATGCTGTGCTGACAGAAGCCGCG  
 ATTACACGGCCAAATACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCCACTG  
 ACCTTCTTCCCAAGATGCGTATGAGCCCTTAACGCCAGTCTTGTAACCTGTCTCTGTGGGACGCCCTCAAGTACC  
 TGGGGAGCCCAATCAAGTCTGAAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCTCT  
 TCGGATACATTCTCTATGAGACAGCATCACTCGTCTGGCATCTCAGTGGCCACGTGCATGATCGGGGGCAGG  
 TGTTTGTGAACACAGTATCCATAGGATTTCTTGGATACACAGCAACCAAGAGATGCTGTCCCTGATCCAGGGT  
 ACACCGTGCTGAGGATCTTGGTGGAGATCGGGGCGAGTCAACTATGGGAGAAATATTGATGACCGACCGCAAG  
 GCTTAATTGGAATCTCTATCTGAATGATTACCCCTGAAAAACTTCAGAATCTATAGCTGGATACCTGCTTTCTCTTGG  
 GCTTCTTCAAGGTTTCAGAGCTGGACCAATGNGTTCCCTCCCAAGAACCCCACTACCTGCTTTCTCTTGG  
 GTAGCTTGTCCATCAGCTCCACGCCCTGTGACACCTTTCTGAAGCTGGAGGCTGGGAGAACCTTACCTGCTTTGATTCA  
 TCAATGGCCAGAACCTTGGACGTTACTGGAACATTGGACCCAGAGAGCGCTTTACCTCCAGGTCCTGGTGA  
 GCAGCGGAATCAACAGGTCATCGTTTTTGGAGGACGATGGCGGCCCTGCAITTAGAGTTACGGAACCCCCC  
 ACTGGGCGAGAACCTGATCACTTAAAGTGAAGGCTGGCACCCTCTCTGCTGGTGCCAGTGGGAGACTGCCGCTC  
 CTCTTGAACCTGAAGCTGTGGTCTGCTGCCACCCCTCACTGCAAAAGCATCTCTTAAGTAGCAACCTCAGGG  
 ACTGGGCGCTCAGCTTGCCTCTGCTCAGCTCAAAACCTTAAGCTTGCAGGGAAGGTGGGATGGCTCTGGGCC  
 TGGCTTTGTTGATGATGGCTTCTTACAGCCCTGCTCTTGTGCGAGGCTGTGGGCTGTCTCTAGGCTGGGAGC  
 AGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAAAGTGTGAAACGTGCCCTTGACCCGGAAGCTCAGAGCCC  
 TGCAGCATCTCTGGACTCAGGCGTGCTTTTGTGCTGTTCTGGGAGGCTTGGCCACATCCCTCATGGCCCAT  
 TTTATCCCGGAAATCTGGGTGTGTCACAGTGTAGAGGCTGGGGAAGGGGTGTCTCACTGAGCTGACTTTGTT  
 CTTCTTCAACACTCTGAGCCTCTTTGGGATTCTGGAAGGAATCTGGCGATGAGAAACATGTGACTTCCCTT  
 TCCCTTCCCACTCGCTGCTTCCACAGGGTGACAGGCTGGGCTGGAGAAACAGAAATCTCACTCGCTGCTTCC  
 CAAGTTAGCAGGTGTCTTGGTGTTCAGTGAGGAGGACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCA  
 CATCCAGGAGGAGGAGCAGAAGGCCAGCTCACAATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCAATCC  
 AGGAGGAGGAGCAGAAGGCCAGCTCACAATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCAATCCAGGGA  
 GGAAGCACAAGGCCAGCTCACAATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCAATCCAGGAGGAGG  
 ACAGAAGGCCAGCTCAGTGCCCTCCCGCTCCCAACCCCAAGCAGGAGGAGGAGCAGGAGGAGGAGGAGG  
 GAAGTGTGTCCAAAGTCGCAATTTGAGCTTGTCTTGGGGCCAGGCCAACACCTGGCTTGGGCTCACTGTCTGTA  
 GTTCAGTAAAGCTATAAACCCTGAATCACAA

## **FIGURE 64**

MTTWSLRRRPARTLGLLLLVVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW  
IFGGSIIHYFRVPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKFDMSGNLDLEAFVLMA  
AEIGLWVILRPGPYICSEMDLGGGLPSWLLQDPGMRRLRTTYKGFTAEVDLYFDHLSRVVPLQ  
YKRGGPPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLLTSDNKDGLSKGIVQGVLAT  
INLQSTHELQLLTTFLEFNVQGTQPKMVMETWTGWFDSWGPFHNILDSSEVLKTVSAIVDAGS  
SINLYMFHGGTNFGFMNGAMHFDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP  
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYIILYE  
TSITSSGILSGHVHDRGQVFVNTVTSIGFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN  
IDDQRKGLIGNLYLNDSPKKNFRIYSLDMKKSFFQRFGLDKWXSLEPETPTLPAPFFLGSLSSIS  
STPCDFTFLKLEGWEKGVVFFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA  
LQFTETPHLGRNQYIK

### **Signal sequence:**

amino acids 1-27

### **Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

### **N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586



## FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC  
 CTGGTGAGGGTTCTCTACTTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGG  
 GGAGCAAAGCCGGGCTCGGCCCGAGGCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC  
 CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAACGCCATGGCTCCC  
 AAGAAGCTGTCTGCCTTCGTTCCCTGCTGTGCGCGCTCAGCCTGACGCTACTGCTGCCCA  
 GGCAGACACTCGGTCTCGTAGTGGATAGGGGTATGACCGGTTTCTCCTAGACGGGGCCC  
 CGTTCCGCTATGTGTCTGGCAGCTGCCTACTTTCCGGGTACCGCGGTGCTTTGGGCCGAC  
 CGGCTTTTGAAGATGCGATGGAGCGGCTCAACGCCATACAGTTTTATGTGCCCTGGAACCTA  
 CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCCTTCTGA  
 ATGAGGCAGCTCTAGCGAACCCTGTTGGTCATACTGAGACCCAGGACCTTACATCTGTGCAGAG  
 TGGGAGATGGGGGCTCTCCCATCCTGGTGTGCTTCGAAAACCTGAAATTCATCTAAGAACCTC  
 AGATCCAGACTTCCTTGCCGCGAGTGGACTCCTGGTTCAAGGCTTGTGCTGCCAAGATATATC  
 CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTGAGGTGGAGAATGAATATGGTAGC  
 TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGGCTCTTCCTGTCACCTGCTAGG  
 AGAAAAGATCTTGCTCTTACCACAGATGGGCTGAAGGACTCAAGTGTGGCTCCCTCCGGG  
 GACTCTATACCAGTGTAGATTTTGGCCACGCTGCAACATGACCAAAATCTTACCCTGCTT  
 CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA  
 CTGGGGCCAGAATCACTCCACACGGTCTGTGTGAGCTGTAAACCAAGGACTAGAGAACATGC  
 TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG  
 AATGGTGGCGATAAGAAGGGACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACC  
 TATATCTGAGCAGGGGACCCACACCTAAGCTTTTTGTCTTTCGAGATGTCATCAGCAAGT  
 TCCAGGAAGTTCCTTTGGGACCTTTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG  
 ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCCTAGACTTGCTTTGCCCCCGTGGGCCCAT  
 TCATTTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC  
 GAACCTATATGACCCATACCATTTTTTGAGCCAACACCATTCTGGGTGCCAAATATATGGAGTC  
 CATGACCGTGCCTATGTGATGTTGGATGGGGTGTTCAGGGGTGTTTGGGAGCGAAATATGAG  
 AGACAAACTATTTTTCAGCGGGGAAACTGGGGTCCAAACTGGATATCTTGGTGGAGAACATGG  
 GGAGGCTCAGCTTTGGGTCTAAACAGCAGTGAATCAAGGGCCTGTTGAAGCCACCAATTCTG  
 GGGCAAAACAATCCTTACCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG  
 GTGGTTTCCCTCCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT  
 ACTCCAAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG  
 ACCAAGGGCCAAAGTCTGGATCAATGGGTTTAACTTGGGCCCGGTACTGGACAAAGCAGGGGCC  
 ACAACAGACCTCTACGTGCCAAGATTCTCTGCTGTTTCTAGGGGAGCCCTCAACAAAATTA  
 CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTGGATAAGCCTATC  
 CTCATAGCACTAGTACTTTGCA CAGGACACATATCAATTCCTTTTACGCTGATACACTGAG  
 TGCCCTCTGAACCAATGGAGTTAAGTGGGCACCTGAAGGTTAGGCCGGGCATGGTGGCTCATGC  
 CTGTAATCCAGCACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTGAGGACTTCAAGA  
 CCAGCCTGGCCAACATGGTGAACCCCGCTCCACTAAAAATACAAAATTAGCCGGGCGTG  
 ATGGTGGGCACCTCTAATCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC  
 AGGAGGCAGAGGTTGCACTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA  
 GACACTCCATCTCAAAAAAAAAAA

## **FIGURE 66**

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFFVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF  
TLLRKYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMYMFHGGTNF  
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFETPFWVFN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSDDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSGVGDFTLYL  
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD  
KPIINSTSTLHRTHINSLSADTLASASEPMELSGH

### **Signal sequence:**

amino acids 1-27

### **N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

### **Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

### **Tyrosine kinase phosphorylation site.**

amino acids 191-198

### **N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## FIGURE 67

GCTTTGAACACGTCTGCAAGCCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC  
ACCCACAATATGGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT  
TTATGGCTTTTATCTGCCTCTACACTCTCTTCTGGTTATTTCAGGATACCTTTGAAGGAATATT  
CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT  
GCGTTCCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCGAAGCGTTTTGGTGTGTT  
CTTGTCAGAAGTTAGTGAAAAATAAACTTAGGGAAATTAGTTTGAACCATGAGTGGACATTTG  
AAAACTCAGGCAGCACATTTACGCAACGCCCCAGGACAAGCAGGAGTTGCATCTGTTTCATG  
CTGTCGGGGGTGCCCGATGCTGTCTTTGACCTCAGACCTGGATGTGCTAAAGCTTGAAC  
AATTCAGAAGCTAAAATTCCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTCTTCGCGATCACTTGAGA  
TGCCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGCTCAAAAA  
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTTGACCAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC  
TAAACTCTTTGGTACTGAACAGCCTTAAGAAAAATGATGAATGTGCTGAGCTGGAACCTCCAGA  
ACTGTGAGCTAGAGAGAATCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACCTGGAT  
TTAAAGTCCAATAACATTTCGCACAATTGAGGAAATCATCAGTTTCCAGCATTTAAAACGACT  
GACTTGTTTAAAAATTATGGCATAACAAAATTGTTACTATTCTCCTCTATTACCCATGTCA  
AAAACCTGGAGTCACTTTATTTCTCTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT  
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTTCATATCACTGGGAACAAAGTGGACATTTCTGC  
CAAAACAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACCTGCATCACC  
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAACTG  
CTTGGACCGCCTGCCAGCCCAGCTGGGCCAGTGTGCGATGCTCAAGAAAAGCGGGCTTGTG  
TGGAAGATCACCTTTTTGATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA  
AATATTCCTTTGCAATGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC  
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG  
ATACATCTTTAAAAATAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT  
GTTCAATGTTTGTAGGTTTAAAGTCATTCAATTTCCAAATCATTTTCTTTTCTTTTGGGG  
AAAGGGAAGGAAAAATTATAATCACTAATCTGGTTCCTTTTAAATTGTTTGAACCTGGAT  
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCTGCTAAGTAAGTAAATGATTAAATTGACATT  
TTCTTACTAAAAA

## **FIGURE 68**

MAYMLKKLLISYISIIICVYGFIGLYTLFWLFRIPLKEYSEKVVREESSFSDIPDVKNDFAFLLHMVDQYDQLYSKRFVFLSEVSENKLRREISLNHEWTFEKLQRHISRNAQDKQELHLFMLSGLVPDAVFDLTDLDVLKLELIFEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLSENKMGLESRLRELRLKILHVKSNTKVPNSITDVAPHLTCLKVIHNDGTKLLVLNSLKKMMNVAEELQNCCELERIPHAIFSLSNLQELDLKSNNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESPLYFSNNKLESPLVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTNLGQNCITSLPEKVGQLSOLTQLELKGNCCLDRLPALGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIPFANGI

### **Signal sequence:**

amino acids 1-20

### **N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

### **Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

### **Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

### **N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

## FIGURE 69

CCCACGCGCTCGGCGCTTCTCTCTGGACTTGCATTTCATTCCATTCCTTTTCATTGACAAATGACTTTTTTTATTTCT  
 TTTTTTCCATCTCTGGGCGAGCTTGGGATCCTAGGCGCGCCTGGGAAGACATTTGTGTTTACACACATAAGGAT  
 CTGTGTTTGGGGTTTCTTCTTCTCTCCCTGCATTTGGCATTTGCTTACTGGTTGTCTGGGGAGGAGACCAGTGG  
 GCTCAGTGTCTGCTTGCATTTCTGCGCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGGCTGTCT  
 ATCGCTGGTGGTATCTCTGGCGGCTTGTCTCCTGCTGATAGTTGCTGTCTCTGTCTTACTTCAAAAATACACAA  
 CGCTAAAAGCTGCAAAAGGACCTGAAGCTGTGGCTGTAAAAAATCACAAACGAGCAAGGTGTGGTGGGCGAAG  
 AACAGCCAGCCCAAAACCATTTGCCACGGAGTCTTGTCTGCCCTGCAGTGTGTGAAGGATATAGAATGTGTGCC  
 AGTTTGTATTCCTGCCACCTTGTGTTTGGCAGATATAATAGGGGCTCTGTAGTTAGGAAAGGCTCCCTTCTCAA  
 GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGCAAGAAGAAAGGCAAG  
 CTCCTCATCAGTTTCATGGAAAAATCACTAGTGCCTGTCTGGGAACAGCTGTCTGGAGATCCCTACAGAGAGCTTC  
 CACTGGGGGCAACCCCTCCAGGAAGGAGTTGGGGAGAGAGAACCTCACTGTGGGGAATGTGATAAAACAGTCA  
 CACAGCTGTCTTATTTCCACACAAATCTACCCCTTGCCTGGCTGGAATGACGTTTCCCTGGAGGTGTCCAGAAA  
 GCTGATGTAAACAGAGCCTATAAAAGCTGTGCTCTTAAAGGCTGCCAGCGCTTGCCTGAGCTGTGTA  
 AGAAGGCTCATGCCATTGACCTCTTAATTCTCTCTGTTTGGGCGAGCTGACATGGCGGAGGCTGAAGGCAAT  
 GCAAGCTGCACAGTCACTTAGGGGGTGCCAATATGGCAGAGACCCACAAAGCCATGATCTTGCACCTCAATCCC  
 AGTGAGAACTGCACCTGGACAATAGAAAGACGAGAAACAAAGCATCAGAAATATCTTTTCTATGTCCAGCTT  
 GATCCAGATGGAAAGCTGTGAAAGTGAACCAATTAAAGTCTTTGACGGAACCTCCAGCAATGGGCGCTGTCTAGGG  
 CAAGTCTGCAGTAAAAACGACTATGTTCTGTATTTGAATCATCATCAGTACATTGACGTTTCAAAATAGTTACT  
 GACTCAGCAAGAAATTCAAAGAACTGTCTTTGTCTTCTACTACTTCTTCTCTCTTAAAGATCTCTATTTCCAACTGT  
 GGGGTTTACCTGGATACCTTGGAAAGATCTTACCAGCGCCCAATTACCACAAAGCGCATCTCTGAGCTGGCTTAT  
 TGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTTAAACTTCAAGAGATTTTCTCTAGAAATAGAC  
 AAACAGTGCAAATTTGATTTTCTTGCATCTATGATGGCCCTTCCACCAACTCTGGGCTGTGTGGACAGTCTGT  
 GGCGGTGTGACTCCCACCTTGAATCGTCATCAAACCTCTCTGACTGTCTGTGTCTAAGATTGCAAGTTTCTCT  
 TACCGGGGATTTTCTGCTTCTTACACCTCAATTTATGACAGAAACATCAACACTATCTTCTTAACTTGCCTCTCT  
 GACAGGATGAGAGTTATTATAAGCAAACTCTACCTAGAGCTTTTAACTCTAATGGGAATTAACCTGCAACTAATAA  
 GACCCAATCTGACAGCAAAATTTATCAATGTTGTGGAATTTCTGTCCCTCTTAATGGATGTGGTACAATCAGA  
 AAGGTAGAAGATCAGTCAATTTTACACCAATATAACACCTTTCTCTGATCTCAACTCTCAACTGTGATCAACC  
 CGTCAGAAACCACTCCAGATTATTTGTGAAGTGTGAATGGGACATATTTCTACAGTGGAGATAATATACATAACA  
 GAAGATGATGTAATACAAAGTCAAATGCACCTGGCAAAATATAACACCAAGCATGGCTCTTTTGAATCCAATTA  
 TTTGAAAGAATATATCTTGAATCACCATATTTGTGGAATTTGAACCAACCTCTTTTGTTCAGTTAGTGTGAC  
 ACCTCAGATCCAAATTTGGTGGTGTCTTGTGATACTGTAGAGCTCTCTCCACCTCTGATCTTGCATCTCCAACC  
 TACGACCTAATCAAGATGTGATGTAGTGGAGTAAACTTGTAAAGTGTATCCCTTATTTGGACATATGGGAGA  
 TTTCCAGTTTGAATGCTTTAAATCTTGAAGATGTAGCTCTGTGTATCTGCAGTGTAAAGTTTGTATATGTGAT  
 AGCAGTGACCACAGTCTCGCTGCAATCAAGGTTGTGTCTCCAGAAGCAACGAGACATTTCTCATATAAATGG  
 AAAACAGATTCCATCATAGGACCCATTCTCTGAAAAGGGATCGAAGTGCAGTGGCAATTGAGGATTCAGCAT  
 GAACACATGCGGAGAAAATCCAAACCGACCTTTCAACAGTGTGATCTGTGTTTCTTTCATGTTCTAGCTCTG  
 AATGTGTGTGATCTGAGGCAATCAGTGTGAGGCAATTTGTAAATCAAGGGGAGACCTCAAAATACCAAGAGCTG  
 CAGAACTATTAACTAACAGGTCCAACCTTAAGTGAGACATGTTTCTCAGGATGCCAAAGGAAATGCTACCTGT  
 GGCTACACATATATGAATAAATGAGGAAGGGCCTGAAAGTGACACAGGCCTGCTATGAAAAAA

## FIGURE 70

MELVRRRLMPLTLLILSCLAEITMAEAEAGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIIRIIFSYVQLDDPGSCSENIKVFDGTSSNGPLLGQVCSKNDYVPVFESSSSLT  
FQIVTDSARIQRTVFVFFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV  
EKDYKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSSSSLTVVLS  
TDYANSYRGFSASYTSIYAENINTTSLTSSDRMRVIIISKSYLEAFNSNGNQLKDPCTCRP  
KLSNVVEFSVPLNGCGTIRKVEDQSIYTNIIITFSASSTSEVITRQKQLQIIIVKCEMGNST  
VEIYITEDDDVIQSONALGKYNTSMALFESNSFEKTILESPPYVDLNLQTLFVQVSLHTSDPN  
LVVFLDTCRASPTSDPASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL  
QCKVLI CDSSDHQSRCNQGCVSRSKRDISSYKWKTDISIIGPIRLKRDRSASGNSGFGHETHA  
EETPNQPFNSVHLFSFMVLALNVVTATITVRHFVNQRADYKYQKLQNY

### Signal sequence:

amino acids 1-24

### Transmembrane domain:

amino acids 571-586

### N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

### Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

### Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

### N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

### Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

## FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG  
 GGACATGCGCGCCCGCAGGAGCTCCCGAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGC  
 TGTGTCGCGCCCGCGCGCTGCCCTGCCACAGCGCCACGCGCTTCGACCCACCTGGGAGTCC  
 CTGGACGCCCCGCCAGCTGCCCGCGTGGTTTGACCAGGCCAAGTTTCGCATCTTTCATCCACTG  
 GGGAGTGTGTTTCCGTGCCCGAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTGGCAAAAGGAAA  
 AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCTCCTAGTTTCAAATATGAAGAT  
 TTTGGACCACTATTTACAGCAAAATTTTTTAATGCCAACAGTGGGCAGATATTTTTTCAGGC  
 CTCTGGTGCCAAATACATTGTCTTAACTTCCAACATCATGAAGGCTTTACCTTGTGGGGGT  
 CAGAAATATTTCGTGGAAGTGGAAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA  
 CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGCTTTTGGACTGTACTATTCCCTTTTTGA  
 ATGGTTTCATCCGCTCTTCTTGGAGATGAATCCAGTTTCATTCCATAAGCGGCAATTTCCAG  
 TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG  
 TCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT  
 ATATAATGAAAGCCAGTTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA  
 TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA  
 CATAAATGGGAAAAGTGCATGACAATAGACAACTGTCTCTGGGGCTATAGGAGGGGAAGCTGG  
 AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTTTCATGTG  
 GAGGAAATCTTTTGATGAATATTGGGCCCACACTAGATGGCACCATTCTGTAGTTTTTGAG  
 GAGCGACTGAGGCAGTGGGGTCTCTGGCTAAAAGTCAATGGAGAAGCTATTATGAAACCTA  
 TACCTGGCGATCCCAGAATGACACTGTACCCCCAGATGTGTGGTACACATCCAAGCCCTAAAG  
 AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCACATCAGGACAGCTGTCTCTTGGCCAT  
 CCCAAAGCTATTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACTG  
 GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCATCAGATGC  
 CGTGTAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG  
 ATGCTGCAAGTTATGTTCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGA  
 AAGCAATGTAACCTGGATAAGAAAAATTATTTGGCAGTTTCAGCCCTTTCCCTTTTCCCCTA  
 AATTTTTCTTAAATTACCCATGTAAACATTTTAACTCTCCAGTGCACTTTGCCATTAAAGTC  
 TCTTCACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAAATTTTTTTCACATTATAGTAG  
 CAAGGAATTGGTGGTATTATGGACCGAACTGAAAAATTTTATGTTGAAGCCATATCCCCATG  
 ATTATATAGTTATGCATCACTTAATATGGGGATATTTTCTGGGAAATGCAATTGCTAGTCAAT  
 TTTTTTTTGTGCCAACATCATAGAGTGTATTTACAAAAATCCTAGATGGCATAGCCTACTTACA  
 CACCTAATTGTATGGTATAGACTGTGCTCTAGGCTACAGACATATACAGCATGTTACTG  
 AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAACATAGAGAAG  
 GTACAGTAAAAAATCTGTAAAAATAAATGGTGCACCTGTATAGGGCACTTACCACGAATGGAG  
 CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCTAGGACATTA  
 TTGAACACTGCCAGACGTTATAAAATACTGTATGCTTAGGCTACACTACATTATAAAAAAA  
 GTTTTTCTTTCTTCAATATAAAATAACATAAGGTACTGTAACTTTACAAACGTTTAAAT  
 TTTAAACCTTTTGGGCTCTTTGTAAATAACACTTAGCTTAAACATAAACTCATTGTGCA  
 ATGTA

## **FIGURE 72**

MRPQELPRLAFPLLLLLLLLLPPPPCPAHSATRFDPWTESLDARQLPAWFDQAKFGIFIHWG  
VFSVPSPFGSEWFWWYQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLFEW  
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDDGAPDQYWNSTGFLAWLY  
NESPVRGTVTVINDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGNNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT  
WRSQNDTVPD VWYTSKPKKEKLVYAIFLKWFTSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKGWGALALTNVI

### **Signal sequence:**

amino acids 1-28

### **N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

### **Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

### **Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

### **N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

### **Leucine zipper pattern.**

amino acids 410-432

### **Alpha-L-fucosidase putative active site.**

amino acids 283-295



## FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT  
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC  
TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG  
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCT  
TTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCCCTGTGAGCAAAAAGGCGAACCCAG  
AGCTGAATTTACAGAAGCTTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG  
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGA  
TGGATTCTGGTGCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG  
TCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTTACAACATCATCTGAT  
ACTTGGACTAACTCGTGCAATTCAGAAAATTATCACCACCAAAGATCCCATATTCAACACTCA  
AAGTGCACAACAAACAACAGAATTTATTGTCAAGTGCAGTACCTACTCGGTGGCATCCCCCTT  
ACTCTACAATACCTGCCCCCTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGG  
AGAAAAAATTTGATTTGTGTACAGAAGTTTTTATGGAACCTAGCACCATTGTCTACAGAAAC  
TGAACCATTTGTTGAAAATAAAGCAGCACTTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC  
CCACGGCTCTGCTAGTGTCTGCTCTCTCTCTTGTGTCTGCAGCTGGTCTTGGATTTTGC  
TATGTCAAAAGGTATGTGAAGGCCTTCCCTTTTACAAAAGAATCAGCAGAAGGAAATGAT  
CGAAACCAAAGTAGTAAAGGGAGAGAAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGA  
AACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCGATGCCTGGAA  
GCTGAAGTTT~~TAGAT~~GAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTTCATGCTCC  
TTACCTTGCCCCAGCTGGGGAATCAAAGGGCCAAAGAACCAAAGAAGAAAGTCCACCCCTT  
GGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAAATGC  
CCTTCTCCTTATTGTAACCCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC  
TTTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTGTCAAAGTGCAA  
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGG  
TGGGTTGAAAGCCAAAGGAGTCACTGAGACCAAGCCTTCTCTACTGATTCGCGAGCTCAGAC  
CCTTCTTCTCAGCTCTGAAAGAGAAAAACGATATCCCACTGCACATGTCTCTGAGCCCGGTA  
AGAGCAAAAGAATGGCAGAAAAGTTTAGCCCCCTGAAAGCCATGGAGATTCTCAAACTTGAG  
ACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACT  
GTCAGCAGGAGCTGTAAACACAGACAGGGTCAAAGTGTCTCTGAAACATTTGAGTTGGA  
ATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCCTGCTGATATTTTCTCT  
AGGAAATATACTTTTACAAGTAACAAAAATAAAACCTTTATAAATTTCTATTTTATCTGA  
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTTAAAGATAATAAAATTC  
ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTCTGTGCAAGGTATTACACTCTGTAAT  
TGAATATTATCTCTCAAAAAATTCACATAGTAGAAGCCTATCTGGGAAGCTATTTTTTCA  
GTTTGTGATATTTCTAGACTTATCTACTTCCAACTAATTTTTTATTTTGTCTGAGACTAATCTT  
ATTCATTTTCTCTAATATGGCAACCATTATAACCTTAATTTTATTATTAACATACCTAAGAAG  
TACATTGTTTACCTCTATATACCAAGCACATTTTAAAAGTGCCATTAAACAAATGTATCACTA  
GCCCTCCTTTTTCCAAAGAAGGAGCTGAGAGATGCAGAAATATTTTGTGACAAAAAATTA  
AGCATTTAGAAAACCT

## **FIGURE 74**

MARCFSLVLLLTISIWTTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTAKEACR  
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGLIWKVPVSRQF  
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP  
APASTSIPRRKKLICVTEVFMETSTMSTETETFFVENKAAFKNAAAGFGGVPTALLVLALLFF  
GAAAGLGFYVKRYVKAFPFTNKNQKEMIETKVVKEEKANDSNPNEESKKTDKNPESKSP  
SKTTVRCLEAEV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

### **Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

### **Tyrosine kinase phosphorylation site.**

amino acids 79-88

### **N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## FIGURE 75

AGATGCGCGTCTTGGCACCTCTAATTGCTCTCGTGATTTCGGTGCCGCGACTTTCACGATGG  
CTCGCCCAACCTTACTACCTTCTGTGCGCCCTGCTCTCTGCTGCCTTCTACTCGTGAGGAA  
ACTGCCGCGCTCTGCCACGCTCTGCCACCCCAACGCGAAGACGGTAACCCGTGTGACTTTG  
ACTGGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA  
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAAT  
TCTTTTCTTCCGCTTGGATATTGCGATGGGCTACTTTACATCACACTCTGCATAGTGTTC  
TGATGACGTGCAAAACCCCCCTATATATGGGCCCCGAGTATATCAAGTACTTCAATGATAAA  
ACCATTGATGAGGAAC TAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTGCCAA  
TTGGTCTAATGACTGCCAATCATTTGCCCCATCTATGCTGACCTCTCCCTTAAATACAAC  
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACATGATGTTAGTACGCGGTAC  
AAAGTGAGCACATCACCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAA  
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTTCTCTG  
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTGAGA  
TGGGGAAAACAAGAAGGATAAAATAAGATCCTCACTTTGGCAGTGCTTCCCTCTCCTGTCAATT  
CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNNATTNATGTTTTCCCTTTGG  
CTGNGACTGGNTGGGCGAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAG  
GCACCCTACAGGAAGGCCTGCCATGCTGTGGCCAACCTGTTTCACTGGAGCAAGAAAGAGATC  
TCATAGGACGAGGGGGAAATGTTTTCCCTCCAAGCTTGGGTGAGTGTGTTAACTGCTTATC  
AGCTATTGAGACATCTCCATGGTTTCTCCATGAAACTCTGTGTTTTCATCATTCTCTTAG  
TTGACCTGCACAGCTTGTTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGGTATAGAA  
CGCTAAGAATTTTCCCCAAGGACTCTTGCTTCTTAAAGCCCTTCTGGCTTCGTTTATGGTC  
TTCATTAAGATATAAGCCTAACTTTGTGCTAGTCTCAAGGAGAAACCTTAAACCACAAAG  
TTTTTATCATTTGAAGACAATATTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAA  
TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCTGGACTTTCAC  
TAACCTCTGACATACTCCCCACACCAGTTGATGGCTTCCCGTAATAAAAAGATTGGGATT  
TCCTTTTG

## **FIGURE 76**

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLRKLPPLCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPYADLSLKYN  
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

### **Signal sequence:**

amino acids 1-48

### **Transmembrane domain:**

amino acids 111-125

### **N-glycosylation site.**

amino acids 165-169, 185-189

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

### **N-myristoylation site.**

amino acids 188-194, 225-231

### **Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99
0	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99

[illegible]

## FIGURE 78

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWKLSENGAPEKDVIVAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFQELFWAWEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR  
HRRLRHYDVFCFATALKGRVYYLEHPEKLTLTAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPVVHPHPNCGPPEFGVRSFGFDPQSRLYGVCYRQH

### Signal sequence:

amino acids 1-17

### Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

### Tyrosine kinase phosphorylation site.

amino acids 137-145

### N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

## FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG**ATG**ATGTGGCGACCATCAGTTCTGCTGC  
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC  
CAGGGGAGGGTGACCAGGCGGGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGGAA  
CTTCAGTACGACCATGAGGCTTTCCTGGGACGGGAAGTGGCCAAGGAATTCGACCAACTCA  
CCCCAGAGGAAAGCCAGGCCCGTCTGGGGCGGATCGTGGACCGCATGGACCGCGCGGGGGAC  
GGCGACGGCTGGGTGTGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGCA  
CATACGGGACTCGGTGAGCGCGGCCCTGGGACACGTACGACACGGACCGCGACGGGCGTGTGG  
GTTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCGGTGAAGAATTTTCATGAC  
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTCGGGACGAGCGGCGTTTCCGGGTGGC  
CGACCAGGATGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCCGAGG  
AGTTCCCTCACATGCGGGACATCGTGATTGCTGAAACCTTGGAGGACCTGGACAGAAACAAA  
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA  
GGAGCCGCGTGGGTGCAGACGGAGAGGCAGCAGTTCGGGGACTTCGGGGATCTGAACAAGG  
ATGGGCACCTGGATGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCAGGACCAAGCCC  
CTGGTGAAGCCAACCACTGCTGCACGAGAGCGACACGGACAAGGATGGGCGGCTGAGCAA  
AGCGGAAATCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGG  
ACCTGACCCGGCACCAACGATGAGCTG**TGA**GCACCGCGCACCTGCCACAGCCTCAGAGGCCCG  
CACAATGACCGGAGGAGGGGCCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCCGAGGAG  
GCAGATGCAGTCCAGGCATCCTCCTGCCCTGGGCTCTCAGGACCCCCCTGGGTGGGCTTC  
TGTCCTGTCAACCCCCAACCCAGGGAGGGGCTGTATAGTCCAGAGGATAAGCAATAC  
CTATTTCTGACTGAGTCTCCAGCCCAGACCAGGGACCTTGGCCCCAAGCTCAGCTCTAA  
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCTT  
GGCCCCAGCCCTCTCTGCCTGGCCTGGCCTGGGACACCTCCTCTCTGCCAGGAGGCAATAA  
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAA

## **FIGURE 80**

MMWRPSVLLLLLLLRHGAQGKSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFLGR  
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETYKMLARDERRFRVADQDGDSMATRE  
ELTAFLHPPEEPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAAWVQTERQQ  
FRDFRDLNKDGHLDGSEVGHVLPFAQDQPLVEANHLHESDTDKDGRLSKAEILGNWNMFV  
GSQATNYGEDLTRHDEL

### **Signal sequence:**

amino acids 1-20

### **N-glycosylation site.**

amino acids 140-144

### **Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

### **N-myristoylation site.**

amino acids 263-269, 311-317

### **Endoplasmic reticulum targeting sequence.**

amino acids 325-330



## FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG  
GCGCGGGCGCGGGGTGCGAGGGGATCCTTGACGCCTCTGTCCCTGTTTCTTTGTGCTCCGAG  
CCTGTCTGTCTGTCTGTTTGGCGCCCCCGCTCCCCGCGGTGCGGGGTTGCACACCGATCTGT  
GGCTTCGTCTGATTTCGCGCGAGGCGCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG  
CGGGTCGTCTGTCTCTCTCTCTGCGCCGCGCCCGGGGATCCGAAGGGTGCAGGGGCTCT  
GAGGAGGTGACGCGCGGGGCTCCGCAACCTGGCCTTGCCCGCATTTCTCCCTCTCTCCAG  
GTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCCGGCTCTCGGCCTCGGTGTG  
TGCTGTCTGTCTGTCGCCGGGGCCCGCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATG  
TTTTACCAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCCAGGGGGCTCCG  
CTCTTGAGGAATTTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG  
GCTGCTGTCCACAGGGGAGTAATCAGCAAACCTCAGGGGACCTGTACGAGTCTATAGCCTACC  
TGCTCGAGAAACTATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGAT  
GGTCTGCTTCTTTCACAGTAACATAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAAACCCGAGAAAGAAACTGG  
CAATAAAGATTGTAAAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGC  
GCCGATTTAATTTACAGAAGAAATTTGTTGGAAAAAGTGCTCTAATGTTGGGAATTGGAACA  
GAAGGACACATGTGGGCTTGTTCAGCCAGTGAAACATCCCAAAATAGAATTTTACTTGAA  
AAACTTTACATCAGCCAAAGATGTTTTGTTTGGCCATAAAGGAAGTAGGTTTCAGAGGGGGTA  
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTTCTACGGTAGATGCTGGA  
GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTTTATGATGGTTGGCCTTCTGATGACAT  
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCA  
AGCCTATCCCTGAAGAACTGGGGATGGTTCAGGATGTACATTGTTGACAAGGCTGTCTGT  
CGGAATAATGGCTTCTCTCTTACCACATGCCCACTGGTTTGGCACCACAAAAATACGTAA  
GCCCTGCTGATACAGCTCTGTGCACATGAACAAATGATGTGCAGCAAGACCTGTTATAACT  
CAGTGAACATTGCTTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCTC  
ATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTGAAATCTCGGACATTGGTGCCAAGAT  
AGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTCAGTTTCACTGACTATAGCACA  
AAGAGAATGTCTAGCTGTATCAGAAACATCCGCTATATAGTGGTGGAAACAGCTACTGGT  
GATGCCATTTCTTCACTGTTAGAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAGAA  
CTTCTTAGTAATTTGTACAGATGGGCAGTCTATGATGATGTCCAAGGCCCTGCAGCTGCTG  
CACATGATGCAGGAATCACTATCTTCTCTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG  
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTTCTTCAAGAGAGTTCACAGGATT  
AGAACCAATTGTTTCTGATGTATCAGAGGCATTGTAGAGATTCTTAGAATCCCAGCAAT  
AATGGTAAACATTTTGACAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAATTTGATT  
CTCATAATACCTGAAATGCTTTAGCATACTAGAATCAGATACAAACTATTAAGTATGTCAAC  
AGCCATTTAGGCAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGTTTACAATTTACAGTGT  
ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAACTCAGGAAAGAGGA  
GATAATGTGGATTAAACCTTAAGAGTTCTAACCATGCTACTAATGTACAGATATGCAAA  
TTCCATAGCTCAATAAAGAAATCTGATACCTTAGACCAAAAAAAAAA

## **FIGURE 82**

MSAAWI PALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLEEFVSY  
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDKADIAFLIDGSFNIGQRRFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAlKEVGFRGGNSNTGKAL  
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVT FVDKAVCRNNGFFSYHMPNWF GTTKYVKPLVQKLC THEQMMCSKTCYNSVNIAPLI  
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTFSTFDYSTKENVLAVI  
RNIRYMSGGTATGDAISFTVRNVFGPIRES PNKNFLVIVTDGQSYDDVQGPAAAAHDAGITI  
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

### **Signal sequence:**

amino acids 1-24

### **N-glycosylation site.**

amino acids 100-104, 221-225

### **Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

### **N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

### **Amidation site.**

amino acids 145-149

## FIGURE 83

GCGCGCGCTCCCGCACCCGCGGCCGCCACCGCGCCGCTCCCGCATCTGCAACCCGAGCC  
 GCGCGCTCCCGCGGGAGCGAGCAGATCCAGTCCGCGCCGACGCGCACTCGGTCCAGTCG  
 GGGCGCGGCTCGCGGCGCAGAGCGGAGATGAGCGGCTTGGGGCCACCTGCTGTGCCTGC  
 TGCTGGCGGCGGCGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTC  
 AAGCCCCGCGCGCTCTCAGTACCCGAGGAGGAGGCCACCTCAATGAGATGTTCCGCGA  
 GGTTGAGAACTGATGGAGGACACGACGACAAAATTGCGCAGCGCGGTGGAAGAGATGGAGG  
 CAGAAGAGCTGCTGCTAAAGCATCATCAGAAAGTGAACCTGGCAAACCTTACCTCCAGCTAT  
 CACAATGAGACCAACACAGACAGGAAGTTTGGAAATAATACCATCCATGTGCACCGAGAAAT  
 TCACAAGATAACCAACACAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTG  
 TGGGAGACGAAGAAGGCGAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC  
 ATGTACTGCCAGTTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCT  
 CTGCACCCGGGACAGTGAGTGTGTGGAGACAGCTGTGTCTGGGGTCACTGCACAAAA  
 TGGCCACCAGGGGCGCAATGGGACCATTCTGTGACAAACAGAGGGACTGCCAGCCGGGGCTG  
 TGCTGTGCCCTTCAGAGAGGCGCTGTCTTCCCTGTGTGACACCCCTGCCCGTGGAGGGCGA  
 GCTTTGCCATGACCCCGCGAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATG  
 GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCTCCTCTGCCAGCCCCACAGCCACAGCCTG  
 GTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGTGCC  
 CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG  
 AGGACCTGGAGAGGAGCTGCAGTGAAGAGATGGCGCTGGGGAGCCTGCGGCTGCCGCGCT  
 GCACTGCTGGGAGGGGAAGAGATTAGATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA  
 ATAGCTAAATTTATTTCCCGAGGTGTGTGCTTTAGCGGTGGGCTGACCAGGCTTCTTCTTACA  
 TCTTCTTCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTTCCAGC  
 TCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGTCTTGGGAGAGTCAGGCAGGTTAAAC  
 TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCCTTACCAGTTGGCAG  
 ACAGCGTGTGTTTACATGAGCTTTGATAATTTGTTGAGGGGAGGAGATGGAAACAATGTGG  
 AGTCTCCTCTGATTGGTTTGGGGAAATGTGGAGAAGAGTGCCTCTTTGCAAAACATCAA  
 CCTGGCAAAAATGCAACAATGAATTTCCACGCAGTTCTTCCATGGGCATAGGTAAGCTG  
 TGCCCTTCAGCTGTGTCAGATGAAATGTTCTGTTTACCCCTGCATTACATGTGTTTATTCATC  
 AGCAGTGTGTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATTC  
 CCTCTCTCAGCACAGCCTTGGGAGGGGGTCAATTGTTCTCCTGTCATCAGGGATCTCAGAG  
 GCTCAGAGACTGCAAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCAT  
 CTGGTTGTGACTCTAAGCTCAGTGTCTCTCCACTACCCACACCAGCCTTGGTGCCACCAA  
 AAGTGTCTCCCCAAAAGAGGAGAAATGGGATTTTCTTGAGGCATGCACATCTGGAATTAAG  
 GTCAAACTAATTTCCACATCCCTCTAAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC  
 AGTGTGGGCGAGCCGCTCTCTTAATGAAGACAATGATATTGACACTGTCCCTCTTTGGCAGT  
 TGCATTAGTAACTTTGAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAACA  
 GTACTTAGGTAATTTGATGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC  
 TGAAGACAATTATCAACCAGTGGAGAAAAATCAACCAGCAGGCGTGTGTGAAACATGGTT  
 GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATAGATGTTTTCAGGTGTA  
 TGGACTGTTGGCCACTGATTTCATCCAGAGTTCTTAAAGTTTAAAGTTGCACATGATTGTA  
 TAAGCATGCTTTCTTTGAGTTTAAATATGATATAAACATAAGTTGCAATTGAAATCAAGC  
 ATAATCACTTCAACTGCAAAAA

## **FIGURE 84**

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ  
HKLRS AVEEMEAEEEEAAKASSEVNLANLP SYHNETNTDTKVGNNTIHVHREIHKITNNQTG  
QMVFSETVITSVGDEEGRRSHECI IDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRDSECCG  
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLC CAFQRGLLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRCPASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV  
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEEI

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

### **Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

### **N-myristoylation site.**

amino acids 202-208, 217-223

### **Amidation site.**

amino acids 140-144

## FIGURE 85

AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACTTACCTCACATCTCTCTGGCTCAGAAGGACTCTG  
 AAGATAACAATAATTTCAGGCCATCCACTCTCTCTTCCCTCCCAAACACACATGTGCATGTACACACACATACAC  
 CACACATACACCTTCTCTCTCTTCACTGAAGACTCACAGTCACTCACTCTGTGTAGCAGCTCATAGAAAGAGACAC  
 TAGAGCCTTAAGGACAGGCTTGGCCATTACCTCTGAGCTCTCTTGGCTTGTGTAGCTCAAAAACATGGGAGGGG  
 CCAGGACCGTGTACTCACACCTGTAATCCCAAGCATTCTGGGAGACCGAGGTGAGCAGATCACTTGTAGGTCCAGGAG  
 TCTGAGACCAAGCTGGCCACATGGAGAAACCCCACTCTCTATAAAAAACAAAAATAGCCAGGAGGTGTGTGGC  
 AGGTGCCTGTAAATCCCACTACTCACAGTGGCTGAGCCAGGAGAATCGCTTGAATCCAGGAGGCGGAGGATGCAGT  
 CAGCTGAGTGCACCGCTGCACCTCCAGCTTGGGTGACAGAATGAGACTCTGTCTCAAAACAAACAAACACGGGAGGA  
 GGGGTAGATACTGCTTCTCTGCAACTCTCTTAACCTCTGACATCTCTTCTTCCAGGGCTGCCCCCTGATGGGGCCCTG  
 GCAATGACTGAGCAGGCCACGGCCACAGGACAGGAAAGAGAGGCAATTTGAGGAGGGCAAGAGTGAACGCCCG  
 GTGTAGAACTGACTGCCCTGGGAGGTTGGTCTCTTGGGCCCTGGCAGGCTGTCTGACCCTTACCTCTGAAAAACACA  
 AAGAGCAGGACTCCAGACTCTCTCTTGTGAATGGTCCCCTGCCCTGCAGCTCCACCAAGGCTTCTGTGGCCCC  
 ACTCTTGTCTAGCTTGGGTGGCTGGTGCCACTGCCACTGTGCCGTGGTACCTGGCATGTTCCCTGCCCCCTCA  
 GTGTGCTGCGAGATCCGGCCCTGGTATACGCCCGCTCGTCTTACCGCGAGGCTACCACTGTGGACTGCAATGA  
 CCTATTCTCAGCGCAGTCCCCCGGCCTCCCCGAGGCACACAGACCTGCTCTGTGAGAGCAACAGCATTGT  
 CCGTGTGGACAGAGTGCAGCTGGGCTTACTGGCCAACTCTCACAGAGCTGGAGCTGCCAGAACAGCTTTTCGGA  
 TGCCCGAGACTGTGATTTCATGCCCTGCCCGAGCTGTGAGCCTGCACCTGAGGAGAACCAAGTACCCCGGCT  
 GGAGAGCACAAGCTTTGCAAGGCTGGCCAGCCTACAGGAATCTATCTCAACCAACCAAGCTGTATCCGCATCGC  
 CCCCAGGGCTTTTCTGGCCTTGCACAATCTGCTGGCTGCACTCACTCAACTGCAAGCTTGTGGGCTTGTAGCAG  
 CGCTGTTTGAATGCTGCCCAACTTGGAGATACTCATGATTGGCGGCAACAGGTAGATGCCATCTCTGGACAT  
 GAACCTCCGCGCCCTGGCCAACTGCGTAGCCTGGTGCTAGCAGGCAATGAACCTTCCGGGAGATCTCCAGCTATG  
 CCTGGAGGGCTGCAAGGCTGGAGAGCCTCTCTTCTATGACAAACAGCTGGCCCGGGTGGCCAGGGCGGCAT  
 GGAACAGGTGCCCGGCTCAAGTTCCTAGACCTCAACAAGAACCCGCTCCAGCGGTGAGGGCGGGGACTTTGTC  
 CAACATGCTGCACCTTAAGAGCTGGGACTGAACAACATGGAGGAGTGGTCTCCATCGCAAGTTTGGCTGGT  
 GAACCTCCCCAGCTGACCAAGCTGGACATCAACAATAAACCCAGGCTGTCTTCTATCCACCCCGCGCTTCCA  
 CCACCTGCCCGAGTGGAGGCTCATGCTCAACAACACGCTCTCAGTGCTTGCACCAAGCAGACGCTGGAGTGC  
 CCTGCCAACCTCGCAGGAGTAGTCTCCACGCCAACCCATCCGCTGTGACTGTGTATCCGCTGGGCCATTCG  
 CACGGGCACCCGCTGTCCGCTTCTGAGCTCGAGCCGAATCCACCTGTGTGGGAGGCTTCGCGACCTCCAGGCTCC  
 GGTCCGTGAGGTGGCCCTTCCGAGTGTGAGGAGTGAACGACCACTGTTTGGCCCTCATCTCCCAAGAGCTTCCCCCAG  
 CCTCCAGGTAGCAGTGGAGAGGACATGGTGTGCTATGGCCGCACTGGCCGAAACCGGACCCGAGATCTCAGT  
 GGTCACTCCAGCTGGGCTTGACTGACCACTGCCATGACAGGCAAGGCTGACCCGAGTACCCGAGGAGGACCT  
 GGAGCTCCGAGGGTGACAGCAGAAAGGCAAGGCTATACACTGTGTGGCCAGAACCTGGTGGGGCTGACAC  
 TAAGACGGTTAGTGTGGTTTGGGCCGTGCTCTCTCCAGCAGGCAAGGCAAGGCAAGGCGCTGGAGCTCCG  
 GGTGACAGGAGCCACCCCTATCACATCTGCTATCTGGGTCAACCCACCCCAACAGAGTGTCCACCAACTCAC  
 CTGGTCCAGTGCTCTTCCCTCCGGGCGCAGGGGCCACAGCTCTGGCCCGCTGCTCTGGGGAACCCACAGCTA  
 CRAATTTAGCCGCTCTCTCAGGCACGAGTACTGGGCTGCTGCAAGTGTCTGATGGCCACCACTCA  
 GTTGGCTTGTGTAGGCGCAGGACCAAGAGGCCACTTCTTGTGCAAGAGCTTAGGGGATGCTCTGGGCTCAT  
 TGCCATCTTGGCTTGGAGGCGGCTCTCCCTCAGCCTGGGCTTCTGGGGCTGGAGTGCCCTTCTGTCCGGGTTGT  
 GTCTGCTCCCTCGTCTGCTCCCTGGAATCCAGGGAGGAAGCTGCCAGATCTCCAGAGGGGAGACATGTTGCC  
 ACCATTGTCTCAAAATCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTACCAA  
 AGAGAAGACTCTGGGCCAGATGCCCTGCCAGGAAGGAGCATGGACCCACGCTTGTAGGCTCGGAGCTGGGC  
 CACAGCAGATGGGGCTTTGTGGCCCTGGGGGTGCTTCTGACGCTTGAAGAAAGTTGCCCTTACTCTCTAGGGTCA  
 CTTCTGCTGCCATTCTGAGGAATCTCCAAGGAACAGGAGGACTTTTGTAGAGCTCTCTGCTCCCTCCCATCTT  
 CTCTTGGCCAGAGGCTTCTGGGCTGCTTGGCTGCTCCCTACTGTGTGCCCGGCTGCAACCCCTTCTCTTCT  
 TCTTCTCTGTGACAGCTCAGTTGCTTGTCTTGTGCTCTGCTGCTCTGGCAGAGGCTGAAGAGGCCATCTCATC  
 CTCGGGGGCTGCCCTCAATGTGGAGTGACCCCAAGCAGATCTGAAGGACATTGGGAGGAGGATGCCAGGAA  
 CGCTCATCTCAGAGCTGGGCTGCATTCCGAGCTGACTTCTTATAGGCAATTTGTGACTTTGTGGAGAA  
 ATGTGTCACTCCCCAACCGAATCACTCTTTCTCTGTTTGTAAAAATAAAAAATAATAATACAAATAAA  
 AAAA

## **FIGURE 86**

MRLLVAPLLLA WAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA  
VPPALPAGTQTLLLLQSNISIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL  
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMNFRPLANLRSVLVLAGMNLREISDYALEGLQSLLESLSFYDNQ  
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIKPFALVNL  
ELTKLDITNNPRLSFIHPRAFHHLPPQMETMLNNNALSALHQQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPPFREMTHCLPLISPRSFPPSLQ  
VASGESMVLHCRALAEPEPIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRVTABEAGLYT  
CVAQNVLGADTKTVSVVVVGRALLQPGRDEGQGLELRVQETHPYHILLSWVTPFNTVSTNLTW  
SSASSLRGGGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS  
CHRALGDRPGLIAIILALAVLLLAAGLAHLGTGQPRKGVGRRPLPPAWAFWGSAPSVRV  
SAPLVLPWNPGRKLP RSSEGETLLPPLSQNS

### **Signal sequence:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 629-648

### **N-glycosylation site.**

amino acids 94-98, 381-385, 555-559, 583-587

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 485-489

### **Casein kinase II phosphorylation site.**

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

### **Tyrosine kinase phosphorylation site.**

amino acids 532-540

### **N-myristoylation site.**

amino acids 15-21, 493-499, 566-572

### **Amidation site.**

amino acids 470-474, 660-664, 692-696



## **FIGURE 88**

MRQTIKVIKIFILIICYTVVYVHNKIFDVDCTVDIESLTGYRTYRCAHPLATLTKILASFYI  
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSIDPVKNDFAFMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQLTKNAQDKLELHFLMLSGIPDVTVPDLVELEV  
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRLALHIKFTDIKEIPLWI  
YSLKLTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI  
NNEGTKLIVLNSLKKMANLTELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIIEIISFQ  
HLHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT  
FLPADIGLLQNLQNLAITANRIETLPPELFPQCRKLRLALHLGNNVLQSLPSRVGELTNLTQIE  
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

### **Transmembrane domain:**

amino acids 51-75 (type II)

### **N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

### **Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

### **N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447



## FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCCGTACTTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT  
CCCGCGTGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACT  
GGCCACAGAGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG  
TTCGTGGTGGCTCTATTATGCCACCAACTCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGGAAATTGGGC  
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT  
GTGGATAATCCCGTGGGCACTGGGTTAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA  
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAG  
AATTCCAGACAGTTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGT  
TGCTTGGGTGATTCTCGGATCTCCCTGTTGATTGCGTGCTCTCCTGGGGACCTTACCTGT  
ACAGCATGTCTCTTCTCGAAGACAAAGGCTCGGCAGAGGTGTCTAAGTTGCAGAGCAAGTA  
CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT  
GATCATGAAACAGAACACAGATGGGGTGAACCTCTATAACATCTTAACATAAAGCACTCCCA  
CGTCTACAATGGAGTCGAGTCTAGAATTACACAGAGGCCACCTAGTTTGTCTTTGTGAGGCG  
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA  
GCTCAAAATATTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGCTTTTGTGAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGTGGAGGCAGGGATC  
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTGAGGAGGCCTG  
GGTGCGGAAACTGAAGTGGCCAGAAGTGCCTAAATTGAGTCAGCTGAAGTGAAGGCCCTGT  
ACAGTGACCCATAAATCTTTGGAAACATCTGCTTTTGTCAAGTCTACAAGAACCTTGCTTTC  
TACTGGATTCTGAAAGCTGGTCATATGGTTCTTCTGACCAAGGGGACATGGCTCTGAAGAT  
GATGAGACTGGTGACTCAGCAAGAAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT  
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCTGTATCT  
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCT  
GGAGGCAATTGGAATATTCTGCTTCTTAAAAAACCTAAGATTTTAAAAAATTGAT  
TTGTTTTGATCAAAATAAGGATGATAATAGATATTAA

## **FIGURE 90**

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPVMMWLQGGPGSSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPFVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTICKNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNGLYRE  
ATELWGKAEMIIIEQNTDGVNFYNILTKSTPTSTMESLEFTQSHLVCLCQRHVRHLQRDALS  
QLMNGPIRKCLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSXKNLAFYWILKAGHMVP  
SDQGDMALKMMRLVTQQE

### **Signal sequence:**

amino acids 1-25

### **N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

### **Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

### **N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

## FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCGA  
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA  
GGGGAGCCTGCGCCTGTGGGATTTCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGTGGG  
CACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG  
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG  
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACCTATGACATTG  
CCTTGGTGAAGCTGTCTGCACCTGTACCTACACTAAACATCCAGCCCATCTGTCTCCAG  
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA  
AGAGGATGAGGCACCTGCCATCTCCCAACACCTCCAGGAAGTTCAGGTCGCCATCATAACA  
ACTCTATGTGCAACCACCTCTTCTCAAGTACAGTTTCCGCAAGGACATCTTGGAGACATG  
GTTTGTGCTGGCAACGCCCAAGGCGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCTT  
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGGCTGTG  
GTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCCTTTGAGTGGATCCAGAAG  
CTGATGGCCAGAGTGGCATGTCCCAGCCAGACCCCTCTGGCCACTACTTTTTCCCTCT  
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTGAGCCCTACCTGAGCCCATGCAGCCTGGGGC  
CACTGCCAAGTCAGGCCCTGGTTCTCTTCTGTCTTGTGTTGGTAATAAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTTCTCAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 92**

MGARGALLLALLLARAGLRKPESQEAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSRLRW  
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPGWMVQFGQLTSMPSFWSLQAYYTRYFVSN  
YLSPRYLGNSPYDIALVKLSAPVITYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDALP  
SPHTLQEVQVAIINNSMCNHLFLKYSFRKIDFGDMVCAGNAQGGKDACFGDSGGPLACNKNG  
LWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQPDPSWPLLFPPLLWALPL  
LGPV

### **Signal sequence:**

amino acids 1-18

### **N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

### **Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

### **N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

### **Amidation site.**

amino acids 33-37

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

### **Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

## FIGURE 93

CCACGCGTCCGCGGACGCGTGGGAAGGGCAGAAATGGGACTCCAAGCCTGCCTCCTAGGGCT  
CTTTGCCCTCATCTCTCTGGCAAAATGCAGTTACAGCCCGAGCCCGACCGAGCGGAGGACGC  
TGCCCCCAGGCTGGGTGTCCCTGGGCGGTGCGGACCCTGAGGAAGAGCTGAGTCTCACCTTT  
GCCCTGAGACAGCAGAATGTGGAAGACTCTCGGAGCTGGTGCAAGGCTGTGTCCGATCCAG  
CTCTCCTCAATACGGAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCC  
CACTGACCCCTCCACACGGGTGCAAAAATGGCTCTTTGGCAGCCGGAGCCCAAGTGCCATCT  
GTGATCACACAGGACTTTCTGACTTGTGTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC  
TGGGGCTGAGTTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGTGAAGGTCCCCAC  
ATCCCTACCAGCTTCCACAGGCCTTGCCCCCATGTGGACTTTGTGGGGGCACTGCAACCGT  
TTTCCCCAACATCATCCTTGAGGCAACGTCCTGAGCCGCAAGGTGACAGGGACTGTAGGCC  
GCATCTGGGGGTAAACCCCTCTGTGATCCGTAAGCGATACAACCTTGACCTCACAAGACGTGG  
GCTCTGGCACCAGCAATAACAGCCAAAGCCTGTGCCAGTTCCCTGGAGCAGTATTTCCATGAC  
TCAGACCTGGCTCAGTTTCATGCGCCTCTTCGGTGGCAACTTTGCACATCAGGCATCAGTAGC  
CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGCGGGAATTGAGGCCAGTCTAGATGTGCACT  
ACCTGATGAGTGCTGGTGCACCAATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG  
GGAACAGGAGCCCTTCTGCACTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT  
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA  
ACACTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCTGCTCTTCGCCCTCAGGTGACAGT  
GGGGCCGGGTGTTGGTCTGTCTCTGGAAGACACCAGTTCCGCCCTACCTTCCCTGCCTCCAG  
CCCCTATGTACCACAGTGGGAGGCACATCCTTCCAGGAACCTTTCCCTCATCAAAATGAAA  
TTGTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCCACCGCCCTTCATACCAGGAG  
GAAGCTGTAACGAAGTTCCCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGC  
CAGTGGCCGTGCCATACCAGATGTGGCTGCACTTTCTGATGGCTACTGGTGGTCAGCAACA  
GAGTGCCCATTTCCATGGGTGTCCGGAACCTCGGCCCTACTCCAGTGTTTGGGGGGATCCTA  
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCGCCCTCTGGCTTCTCAACCCAAAG  
GCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAACCCGTGGCTGCCATGAGTCTCTGT  
TGGATGAAGAGGTAGAGGGCCAGGGTTTCTGCTCTGGTCCGGCTGGGATCCTGTAAACAGG  
TGGGGAACACCAACTTCCAGCTTTGCTGAGAGACTCTACTCAACCCCTGACCCCTTCTCTATC  
AGGAGAGATGGCTTGTCCCCCTGCCCTGAAGCTGGCAGTTCACTCCCTTATCTGCCCTGTTG  
GAAGCCCTGTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA  
TGCTGTGAGCTTGACTGACTCCCAACCTACCATGCTCCATCATACTCAGGTCTCCCTACT  
CCTGCCCTTAGATTCCTCAATAAGATGCTGTAACCTAGCATTTTTTGAATGCCTCTCCCTCCGC  
ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGTTGTATACAGACTCTGTGCACTA  
TTTCACTTGATATTCATCCCCAATTCAGTGCAAGGAGACCTCTACTGTACCGTTTACTCT  
TTCCTACCTGACATCCAGAAACATGGCCTCCAGTGCATACCTCTCAATCTTTGCTTTATG  
GCCTTTCCATCATAGTTGCCCACTCCCTCTCCTTACTTAGCTTCCAGGTCTTAACTTCTCTG  
ACTACTCTTGCTCTCTCTCATCAATTTCTGCTTCTTCATGGAATGCTGACCTCATTTG  
TCCATTTGTAGATTTTGTCTCTTCTCAGTTTACTCATTTGCCCTGGAAACAAATCACTGACA  
TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAA  
TGTAAAAAA

## **FIGURE 94**

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS  
ELVQAVSDPSSPQYGYKYLLENVADLVRPSPLTLHTVQKWLLAAGAKCHSVITQDFLTCWL  
SIRQAELLPLGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGHLRFPPTSSLRQRP  
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG  
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMASAGANISTWVYSSPGRHEGQEPFLQWLML  
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH  
QFRPTFPASSPYVTVVGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP  
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG  
RPPLGLFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

### **Signal sequence:**

amino acids 1-16

### **N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

### **Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

### **Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

### **N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

## FIGURE 95

GCCGCGCGCTCTCTCCCGGCGCCACACCTGTCTGAGCGGCGCAGCGAGCCGCGGCCCGGGC  
GGGCTGCTCGGCGCGGAACAGTGCTCGGCATGGCAGGGATTCCAGGGTCTCTTCTCTCTC  
TTCTTTCTGCTCTGTGCTGTTGGGCAAGTGAGCCCTTACAGTGCCCTTGAAACCCACTTG  
GCCTGCATACCGCTCTCCCTGTGCTCTTGCCCCAGTCTACCTCAATTTAGCCAAGCCAGACT  
TTGGAGCCGAAGCCAAATTAGAAGTATCTTCTTCATGTGGACCCAGTGTCATAAGGGAAT  
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG  
CAGCCGCACAGAGACGCAGGTGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCCCAAC  
ACCGAGACTCAGGGTCTTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTTATGGCTATGACAGC  
AGGTTTCAGCATTTTTGGGAAGGACTTCCTGCTCAACTACCTTTCTCAACATCAGTGAAGTT  
ATCCACGGGCTGCACCGGCACCCTGGTGGCAGAGAAGCATGTCCTCACAGCTGCCACTGCA  
TACACGATGAAAAACCTATGTGAAAGGAACCCAGAAGCTTCGAGTGGGCTTCCTAAAGCCC  
AAGTTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCCGAGCAGATGAA  
ATTCAGTGGATCCGGGTGAAACGCACCCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA  
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACCTCAAAAAGCCCCACAAGAGAAAA  
TTTATGAAGATTGGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGGCAGAATTCATTCTC  
TGGTTATGACAATGACCGACCAGGCAATTTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA  
CCTATGACTTGCTCTACCAGCAATGCGATGCCCAGCCAGGGGCCAGCGGGTCTGGGGTCTAT  
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGGAGCGAAAAATTATTGGCATTTTTTCAGG  
GCACCAAGTGGGTGGACATGAATGGTTCCTCCACAGGATTTCAACGTGGCTGTGAGAATCACTC  
CTCTCAAATATGCCAGATTTGCTATTTGGATTAAAGGAACTACCTGGATTGTAGGGAGGGG  
TGAACACAGTGTTCCCTCCTGGCAGCAATTAAGGGTCTTCATGTTCTTATTTTAGGAGAGGCC  
AAATGTTTTTTTGTCATTGGCGTGACACCGTGTGTGTGTGTGTGTGTGTGTGAAGGTG  
CTTATAATCTTTTACCTATTTCTTACAATTGCAAGATGACTGGCTTTACTATTTGAAAACTG  
GTTTGTGTATCATATCATATATCATTAAAGCAGTTTGAAGGCATACTTTTGCATAGAAATAA  
AAAAAACTGATTTGGGGCAATGAGGAATATTTGACAATTAAGTTAATCTTCACGTTTTTG  
CAAACTTGATTTTTATTTCATCTGAACCTGTTTCAAAGATTATATTAATAATTTGGCATA  
CAAGAGATATGAAAAAAAAAAAAAAAAA

## **FIGURE 96**

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAELKLEVS  
SSCGPQCHKGTPLPITYEAKQYLSYETLYANGSRTETQVGIIYLSSSGDGAQHRDSGSSGKS  
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAACIHDGKTYVKG  
TQKLRVGFLLPKPKFDGGRGANDSTSAMPEQMKFQWIRVVRTHVPKGIKGNANDIGMDYDYA  
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFGDVKDETYDLLYQQCD  
AQPASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW  
IKGNYLDCREG

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 93-97, 207-211

### **Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

### **Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

### **N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

### **Serine proteases, trypsin family, histidine active site.**

amino acids 171-177



## FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTTT  
CTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCTGTGCTGCTG  
GCGTCGACAGCCATCTCTCAATGCGGCCAGGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCA  
GCAGCTGAACCGGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC  
ACTGTGCGCCACTGTTTCAAGGACAACCTGAACAAACCATACTGTCTCTGTGCTGCTGGG  
GGCCTGGCAGCTGGGGAACCTTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC  
CCCACCCTGTGTATTCTTGAAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGTCTTGCCCATCTGCCTACCTGATGCCTCTATCCACCT  
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCTTGC  
CCCACCCTCAGACCCTGCAGAAAGTGAAGGTTCCTATCATCGACTCGGAAGTCTGCAGCCAT  
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT  
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG  
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCC  
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA  
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG  
CCGCGCGCTCCTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA  
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCGCCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCCCGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCCGAC  
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCCGCCCAACGGCCTCATGTCCCCGCCCCAC  
GACTTCCGGCCCCGCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTTAT  
AGGTATTTGTAAACCTGCCACATATCTTATTTATTCTCCAATTTCAATAAATATTTATT  
CTCCAAAAA

## **FIGURE 98**

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLLASTAILNARIPVPPACGKPPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLTTSRVVITAAHCFKDNLNKPYLFVLLGAWQLGNPGSRSQKVGVA
WVEPHFVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMC
QVDGAWLLAGIISWGECAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS
```

### **Signal sequence:**

amino acids 1-32

### **N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

### **Glycosaminoglycan attachment site.**

amino acids 826-830

### **Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

### **Tyrosine kinase phosphorylation site.**

amino acids 607-615

### **N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## FIGURE 99

GACGGCTGGCCACC**ATG**CACGGCTCCTGCAGTTTCTGTGCTGCCGCTACTGCTA  
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGT  
GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCGACGGCCTCAGACATGCTGCACATGA  
GATGGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCAC  
AACAGGAGCGCGGGCGCCGCGGAGAAATCTGTTGCCATCACAGACGAGGGCATGGACGT  
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT  
GCAGCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC  
GGCTGTGGTTCCTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT  
GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC  
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC  
CCGGAAGATGCTCAGGATTTCCTTACCTGGTAACTGAGGCCCATCCTTCCGGGCGACTGA  
AGCATCAGATCTTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT  
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCTGTGTGGAACCCAGGCC  
CCAACTTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC  
AACTGAGGTCCCTTCATTTTGGCAGCTCACAGCCTGCCCTCCTTGATGAGGAGCCAGTTA  
CCTTCCCCAAATCGACCCATGTTCCCTATCCCAAATCAGCAGACAAAGTGACAGACAAAACA  
AAAGTGCCCTCTAGGAGCCAGAGAACTCTTGGAACCCCAAGATGTCCCTGACAGGGGCAAG  
GGAACTCCTACCCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTG  
AGGTCTTGCCCTCAGTTTTTCCAGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTTCCCCAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGCCCTGACA  
AGCCTAGCGTGTGTGCAGGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA  
CTACTGCTCCTGCCTCCTCTGGTGTGAGTCTTCCCAACCTGTCCCCAGCCCCATAACAAGG  
TGAAGAGGTGAGCTGTCTCCTGTGCATCTTCCCCACCTGTCCCCAGCCCCATAACAAGGATA  
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCC  
ATCCTGGAGGCACAAGGCCCTGGCTGGCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACC  
GGGCCACACCTCTCCTGCCCCCTCCTCCTGAGTCTGGGGGTGGGAGGATTTGAGGGAGCT  
CACTGCCTACCTGGCTTGGGCTGTCTGCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG  
TGAGCTGGGGATGGGATTCCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC  
TTTGAGTGGGGGAGGCAGGGACGAGGGAAGGAAAGTAACCTCTGACTCTCCAATAAAAACCT  
GTCCAACCTGTGA

## **FIGURE 100**

MHGSCSFLMLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLRYAQVSPTASDMLHMRWDEE  
LAAPAKAYARQCVWGHNKERRRGENTFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ  
MCGHYTQVWAKTERIGCGSHFCEKLQGVETNIELLVCNYPGNVKGKRPYQEGTPCSQC  
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRAEASDSRKMGTTPSSLATGIPAFVLTEV  
SGSLATKALPAVETQAPTSLATKDPSPMATEAPPCVTTTEVPSILAAHSLPSLDEEPVTFPKS  
THVIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEALPPSSEVLAS  
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSSLPGAEGPDKPSVV  
SGLNSGPGHVGPLLGLLLLPLVLGIF

### **Signal sequence:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

### **Glycosaminoglycan attachment site.**

amino acids 439-443

### **Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

### **N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

### **Amidation site.**

amino acids 82-86, 172-176

### **Peroxidases proximal heme-ligand signature.**

amino acids 287-298

### **Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

### **Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

# FIGURE 101

GTAAC TGAAGT CAGGCTTTTCATT TGGGAAGCCCCCTCAACAGAAATTTCGGTCATTCTCCAAGTTATGGTGGACGT  
 ACTTCTGTGTGTTCTCCCTCTGCTTGCCTTTTCACATTAGCAGACCGGACTTAAGTCAACAACAGATTATCTTTTCAT  
 CAAGGCAAGTTTCCATGAGCCACCTTCAAAGCCTTCGAGAAGTGAAACTGAAACAACAATGAATTGGAGACCATTC  
 AAATCTGGGACCAGTCTCGGCAAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTGTTGAAATTAATCCCTGA  
 ACATCTGAAAGAGTTTTCAGTCCCTTGGAACTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAAACTGCATT  
 TCCAGCCCTACAGCTCAAAATATCTGTATCTCAACAGCAACCGAGTACATCAATGGAACCTCGGGTATTTTGACAA  
 TTTTGGCCAACAACCTCTTGTGTGTTTAAAGCTGAACAGGAAACCGAATCTCAGCTATCCCACCAAGATGTTTAAACT  
 GCCCACAATGCAACATCTCGAATTTGAACCGAAACAGAGTTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGG  
 TGCTCTGAAGTCTCTGAAAAATGAAAGAAATGGAGTAAACGAAACTTATGGATGGAGCTTTTGGGGGCTGAGCAA  
 CATGGAAATTTTCAGCTTGACCATAAACCACTTAACAGAGATTACCAAGGGCTGCTTTACGGCTTGTCTGATGCT  
 CGAGAGCTTTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCTCGGGAGTCTCTCCGGAAGCTCAG  
 TGAGCTGGACCTAACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTCTGGCCTAAGCTTACTAAATAC  
 ACTGCACATTTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCCTTCGGGGGCTTCCAGTTTAAAGACTTT  
 GGATCTGAAGAACAATGAAATTTCCCTGGACTATTGAAGACATGAATGGTGTCTTCTCTGGGCTTGACAACTGAG  
 GCGACTGATACCTCAAGGAAATCGGATCCGTTCTATTACTAAAAAGGCTTCACTGGTTTGGATGTCATTTGAGCA  
 TCTAGACCTGAGTGACAACGCAATCATGTCTTTTCAAGGCAATGCACTTTTCAAAATGAAGAACTGCAACAAT  
 GCATTTAAATACATCAAGCCTTTTGTGCGATTGGCAGCTTAAATGCGCTCCCAAGTGGCTGGCGGAAACCACTT  
 TCCAGAGCTTTGTAATGCGACTTGTGCCCATCCTCAGCTGTCTAAAGGAGAGAGCAATTTTGTCTGTAGCCGAGA  
 TGGCTTTGTGTGTGATGATTTTCCCAAACCCAGATCAGGTTTTCAGCGAACAACAGCTCGGCAATAAAGGTTT  
 CAAATTTGAGTTTCTCACTCTCAGCTGCCACGACAGTGTATTCCTCAATGACTTTTCTGGGAAAAAGACAATGA  
 ACTACTGCAATGATGCTGAAATGGAATAATATGACACCTTCGGGGCCCAAGGTGGCAGGTGATGGAGTATACCA  
 CATCTCTCGCTCGCGAGGTGGAATTTGCGAGTGGGGGAAATATCAGTGTCTCAATCTCAATCACTTTGTTT  
 ATCTACTCTCTGTCAAAGCCAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCAT  
 CCGAGCTGGGGCATGCGCAGCTTTGGAGTGTGCTGTGTGGGGCACCCAGCCCCAGATAGGCTGGCAGAGGA  
 TGGGGGACAGACTTCCAGCTGCACGGGAGAGACGCATGCAATGTGATGCCCGAGGATGACGTGTGTTCTTTATCGT  
 GGAATGAAGATGAGAGCACTTGGGTATACAGCTGCACAGCTCAGAACAAGTGCAGGAAGTATTTCAAGCAATGCG  
 AACTCTGACTGTCTTAGAAACACCAATCATTTTTCGGGCCACTGTGTGACCGCAACTGTAAACAAAGGGAGAAACAGC  
 CGTCTCAGATGCAATGCTGGAGGAAGCCCTCCCTTAAACTGAACTGGACCAAAAGATGATAGCCCATTTGGTGGT  
 AACCAGAGGCACTTTTTCGACAGGCCAATCAGCTTCTGATTATGTGGACTCAGATGTCAAGTGTGCTGGGAA  
 ATACACATGTGAGATGTTCAACACCTTGGCACTGAGAGAGGAAACGTCGCCCTCAGTGTGATGCCCATCTCAAC  
 CTGCGACTCCCTCAGATGACAGCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTGCTGTGATCATAGC  
 CGTGGTTTGTCTGTGTGGTGGGCACTGCTGCTGTGGGTGGTCTATCATATACCAACAAGGCGGAGGAATGAAGA  
 TTGCAAGTATCAACAACAGATGAGACCAACTTGCAGCAGATATTCCTAGTTATTTGTCACTCAGGGAACGTT  
 AGCTGACAGGCAAGGATGGGTACGTGTCTTCAGAAAGTGAAGCCACCAAGCTTTGTCACTCATCTTCAGGCTGTGG  
 ATTTTCTTACCAACAATGACAGTAGTGGGACCTGCCATATGACAAATAGCAGTGAAGCTGATGTGGAGCTGC  
 CACAGATCTGTTCCTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTGGAAGGAAATGTGATGGCTCAGA  
 TCCCTTTGAAACATATCATACAGTTGTGAGTCTGACCCAGAAGAGTTTAAATGGACCACTTAGAGCCAGTTA  
 CATAAAGAAAAAGGAGTGTACCCATGTTCTATCTTCAAGAAGATCTGTGCAAGCGAGCTTCAGTAAATGATGCT  
 GTGGCTTCACTGTGAGGAAGCTACTTAAACATAGTTACTCTCACAATGAAGGACCTGGAATGAAAACTGTGTG  
 TCTAAACAAGTCTCTTAGATTATTGTGCAAAATCCAGGCCAGCGTGGTTCCTCAGTAACTTCTCATGGG  
 TACCTTTGAAAGAGCTCTCAGGAGACCTCACTTAGATGCTTCAAGCTTTGGACAGCCATCAGATTGTGACGCC  
 AAGACCTTTTATTTGAAAGCTCACTTCTCCAGACTTGGACTCTGGGTGAGGAAGATGGGAAGAGATGAGAC  
 AGATTTTCAGGAAGAAAAATCACAATTGTACTTTTAAACAGACTTTAGAAAACCTACAGGACTCAAAATTTTCAGTC  
 TTAGCTTTGGACATACATAGACTGAATGAGACCAAGGAAAGCTTAACTACATCTCAAGTGAACCTTTTATTTA  
 AAAGAGAGAGAACTTATGTTTTTTAAATGGAGTTATGAATTTTAAAGGATGAAATGCTTTATTTATACAGAT  
 GAACCAAAATTAACAAAGTTATGAAAAATTTTATACCTGGGAATGATGCTCATATAAGAACTCTTTTAAACTA  
 TTTTAACTGTTTGTATTGCAAAAAAGTATCTTACGTAAATTAATGAATAAATCATGATATTTTATGATTTT  
 TTTAATGGCAGATTCTTTTATGGAATAAGTATTACTAAAGCACTTAAATTAATGCTCTGTACCACTTTT  
 TAAATAGAAGTTACTTCAATATATTTTGCACATATATTTTAAATAAATGTGTCAATTTGAA

## FIGURE 102

MVDVLLLFSLCLLFHISRDLNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSN  
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAPFALQLKYLVLNSNRVTSMEP  
GYFDNLANTLLVLKLNRRISAIIPKMFKLPLQHLLELNRRNKIKNVDDLTFQGLGALKSLKM  
QRNGVTKLMDGAFWGLSNMEILQLDHNLLTEITKGWLYGLLMLQELHLSQNAINRISPDAWE  
FCQKLSLDELTFNHLRLDDSSFLGLSLNLTNLHIGNNRVSYIADCAFRGLSSSLKTLDDLKNEE  
ISWITBDMNGAFSGLDKLRLLIQQGNRIRSIITKKAFPTGLDALEHLDDLSDNAIMSLQGNFASQ  
MKKLQQLHLNLTSSLLCDCQLKWLPLQWVAENNFQSFVNASCAPHQLLKGRSIFAVSPDGFVCD  
DFPKPQITVQPETQSAIKGSNLFSICSAASSSDSPMTFAWKKNELLHDAEMENYAHRAQG  
GEVMEYTTILRLREVEFASEGKYQCVISNHFSSYSVKAKLTVMNMLPSFTTKTPMDLTIRAGA  
MARLECAAAGVHPAQIAWQKDGDTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN  
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTER  
HFFAAGNQLLIIVSDSDVDAGKYTCESMNTLGTERRGNVRLSVIPTPTCDSPQMTAPSLDDDG  
WATVGVVIIAVVCCVVGTSVLVWVVIYHTRRRNEDCSITNTDETNLPAIDIPSYLSSQGTAD  
RQDGYVSSSESGHHQFVTSSGAGFFLPQHDSSGTCHIDNSSADVEAATDLFCPLFGSTGP  
MYLKGNVYGSDPFETYHTGCSDPDRPTVLMHDHYEPSYIKKKECYPCHSPSEESCERSFSNLSW  
PSHVRKLLNTSYSNNEGPGMKNLCLNKSSLDFAANPEPASVASSNSFMGTFGKALRRPHLDA  
YSSFGQPSDCQPRAFYLKAHSSPDLDGSGSEEDGKERTDFQEENHICTFKQTLNRYTPNFQS  
YDLDT

### Signal sequence:

amino acids 1-19

### Transmembrane domain:

amino acids 746-765

### N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

### Glycosaminoglycan attachment site.

amino acids 826-830

### Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

### Tyrosine kinase phosphorylation site.

amino acids 607-615

### N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879



## **FIGURE 104**

MLNKMTLHPQQIMIGPRFNRALFDPLLVLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVDPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELEFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPLRLDLGELKRLS  
YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLELDLSGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL  
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE  
LKCRASSTLSVSWITPNGTVMTHGAYKVRIAVLSDGTNLNFTNVTQDTGMYTCMVSNVGN  
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDDNNVGTPVVDWETINVTTSITPQ  
STRSTEKFTTIPVTDINSIGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN  
HHAPTRTVEIINVDEITGDTPMESHLMPAIEHEHLNHNYSYKSPFNHTTTVNTINSIHSS  
VHEPLLIRMNSKDNVQETQI

### **Signal sequence:**

amino acids 1-44

### **Transmembrane domain:**

amino acids 523-543

### **N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

### **Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

### **N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537





## FIGURE 106

MSAPSLRARAAGLGLLLCVILGRGRSDSGRGELGQPSGVAAERPCPTTCRCLGDLDDCSR  
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAIT  
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPAQLKYLVLNSNRVTSMEPGY  
FDNLANTLLVLKLNRRNRISAIPPKMEKLPQLQHLELNRNKIKNVDGTLFQGLGALKSLKMQR  
NGVTKLMDGAFWGLSNMEIQLDHNHNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWFC  
QKLELDTLTFNHLRLDDSSFLGLSLNLTLLHIGNNRVSYIADCAFRGLSSLKTLDLKNNNEIS  
WTIEDMNGAFSGLDKLRLLILQGNRIIRSTTKKAPTGLDALEHLDSLDAIMSLQGNAPSQMK  
KLQQLHLNLTSSLLCDCQLKWLFPQWVAENNFQSPVNASCAHPQLLKGRSIFAVSPDGFVCDFF  
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELHDAEMENYAHLRAQGG  
VMEYTTILRLREVEFASGKYQCVISNHFSSSYSVKAKLTVNMLPSFTKTPMDLTIKAGAMA  
RLECAAVGHPAPQIAWQKDGDTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA  
GSISANATLTVLETPSFLRPLLDRTVTVKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTERHF  
FAAGNQLLIIVDSVDSDAGKYTCMSNTLGTERRGNVRLSVIPTPTCDSPQMTAPSLDDDGWA  
TVGVVIAVCCVVGTSVLVWVVIYHTRRRNEDCSIINTDETNPADIPSYLSSQGTLDADR  
DGYVSSSESGSHHQFVTSAGAGFFLPQHDSSGTHIDNSSADVEAATDLFLCPLFGSTGPMY  
LKGNVYGSDFPFTYHTGCSDDPRTVLMDHYEPSYIKKKECYPCSHPSSESCERSFSNISWPS  
HVRKLLNTSYSHNEGPGMKNLCLNKSLLDPSANPEPASVASSNSFMGTGKALRRPHLDAYS  
SFGQPSDCQPRAFYLKAHSSPDLDSSGEEDGKERTDFQEEHNHICTFKQTLNRYRTNPFQSYDLDT

### Signal sequence:

amino acids 1-27

### Transmembrane domain:

amino acids 808-828

### N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,  
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

### Glycosaminoglycan attachment site.

amino acids 886-890

### Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,  
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,  
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,  
1073-1077, 1079-1083, 1081-1085

### Tyrosine kinase phosphorylation site.

amino acids 667-675

### N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

### Leucine zipper pattern.

amino acids 58-80, 65-87

# FIGURE 107

CAAAACCTTGCCTGCGGAGAGCGCCAGCTTGAATTGAATGGAAGGAGCCCGAGCCCGGGAGCGCAGCTGAGAC  
 TGGGGGAGCGCGTTTCCGCTCTGCGGGCGCCCTCGCGCCCGGGGCGCAGCAGGGGAAGGGGAAGCTGTGGTCTGCC  
 CTGCTCACGAGGCGCCATGCTGGTGTGAACCGGGAGAGCCCTGGTGGTCCCGTCCCTATCCCTCTTTATATA  
 GAAACCTTCCACATCTGGGAAGGCGAGCGCGAGGCGAGGGGCTCATGGTGAAGAGGCGCGGCTGATCTGCAG  
 GGCACAGCATTTCCGATTACAGATTTTACAGATTTTACAGATACCAAATGGAAGGCGAGGAGGCAGAACAGCCTGTGCCTGGT  
 TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGCAAGGCACATGTGCCCAGAGCCGGGTGTGC  
 TGCTCTGTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCTTGGCGTGGAGGCGCCAGGATTTGGCCGAA  
 GTGGCGGCCACAGCTGAGCCCGAAGAGAACAAATTTGCGGAGGAGGAGCGGTGTGTTACTGAGCCCTGAGG  
 AGCCCGGGCTGGCCAGCGCGGCTCAGCTGCCCCGAGACTGTGCTGTGTCCAGGAGGGCGCTGTGGACTGTG  
 CGGTATTGACCTTGCCTGAGTTCGCCGGGACCTGCCCTGAGCACACCAACCTATCTCTGCAGAAACCAACGAGC  
 TGGAAAGATGTACCTTGGAGAGCTCTCCCGGCTGCACCGGCTGGAGACACTGAACTGCCAAACCAACCGCTGA  
 CTTCCCGAGGGCTCCAGAGAAAGCGCTTGTAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAAATAACAAGC  
 TGACCTTGGCACCCTGCTTCTGCCAAACGCGCTGATCAGTGTGGACTTTGCTGCCAACTATCTCAACCAAGATCT  
 ATGGGCTCACCTTTGGCCAGAAGCCAACTTGAAGTCTGTGTACTGCACAAACCAAGCTGGCAGAGCGCCGGC  
 TGCCGGACAACATGTTCAACGGCTCCAGCAACGTTCGAGGTCTCTATCTGTCCAGCAACCTTCTGCGCCACGTGC  
 CCAAGCACCTTGGCGCTGCCCTGTACAGCTGCACCTCAAGAACCAACAGCTGGAGAGATCCCGCCGGGGCTC  
 TCAGCAGCTTGAGCAGCCTGCGGAGCTATACCTGCAGAACCACTACCTTGACTGACGAGGGCTGGACAACGAGA  
 CCTCTGGAAGCTCTCAGCCCTGGAGTACTTGGATCTGTGCAGCAACCACTGTCTCGGGTCCCACTGGGCTGC  
 CGCGCAGCTTGGTGCTGCTGCACTTGGAGAAGAACGCCATCCGAGCGTGGACGCGAATGTGCTGACTGACCCATCC  
 GCAGCTTGGAGTACCTGTCTGCTGCACAGCAACCACTGCGGGAGCAGGCGATCCACCCCTTGGCCTTCCAGGGC  
 TCAAGCGGTGTGACACCGCGAGCCCTGGGCGCCCGTGGCTGGACCTCGCCATCTGCAGCTCTGCGCTGGACA  
 GCACCTCATGATCTCTGCACACCAAGATCAGAGCATTGGCGCGTGGCCACCTTCTGCTGAGG  
 AGCTCAACCTCAGCTACAAACCGCATCAGGCCACAGGTGCACCGCGAGGCTTGGCCACCACTTCTCTTGGAGG  
 GCTCGCTGGAGCTGTGCGCCCAACCGCTGCACACGCTGCCACTGGGCTGCTGAAATGTCTGCTGTGAAGG  
 TCAAGCGCATAGCTGGCTGCCCTGGCAGCAGGGGGCGTGGCGGGCATGGCTCAGCTGCTGAGCTGTACCTCA  
 CCAGAACCCGACTGGCCAGCGGAGCCCTGGGCGCCCGTGGCTGGGAGCTTCTTCTCAGGTTCCTGGACA  
 TCGCCGGGAATCAGCTCAGCAGAGATCCCCAGGGGGCTCCCGAGTCACTTGAATACCTGTATCAGGTCAACCA  
 AGATTGTGCGGTGGCCGCAATGCCCTTGCACCTCAGCCCACTCAAGGGGATCTTCTCAGGTTCACCAAGC  
 TGGCTGTGGGCTCCGTGGTGGACAGTGCCCTCCGAGGGCTGAAGCAGCTTGCAGGTCTTGGACATTGAAGGCACT  
 TAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGAAGGAAAGGAGGAGGAGGAGGAGGAGGAGG  
 AGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAAGTGTGACCTAGGATGATGGACCGCCGAGCTCTTTTCTGC  
 AGCACACGCTGTGTGCTGTGAGCCCCCACTCTGCCGTGCTCACACAGACACCCAGCTGCACACATGAGGCA  
 TCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTTCCACGCGGTGTCCACGGCCAGACACATGC  
 ACACACATCACACCTCAAACACCCAGCTCAGCCACACAACTACCTCCAAACCAACACAGTCTCTGTGTACGAA  
 CCCCCTACCGCTGCCACGCGCTCTGAATCATGACGGGAAGGGTGTGCCCTTGCCTGGGCACACACAGGCCACCA  
 TTTCCCTCCCGTGTGACATGTGTATGCTATGCATACACACACACACACACATGACCAAGATCATGTGCGAA  
 CAGCCCTCCAAAGCTATGCCACACAGCTCTTGGCCACGCCAGATCAGCCATAGCAGCTTCGCGCTGTGCCCT  
 GTCCATCTGTGCTCGTCCGTCCCTGGAGAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCCTGCCACCTCT  
 GGAATCACAAGAGCTGGCTTTTATCTCTTCCATCTCTATGGGACAGGAGCCTTCAAGGATCTGTGGCTTGGCC  
 TGGCCACCCCTCTCTCCAGGTGTGGGCACTCACTCTGCTAAGAGTCCCTTGGCCACCGCCCTGGCAGGACA  
 CAGGACCTTTTCCAATGGGCAAGCCAGTGGAGGACAGGATGGGAGAGCCCTGGGTGCTGTGCGGGCTTGGGG  
 CAGGAGTGAAGCAGAGTGTATGGGCTGGCTGAGCCAGGAGGAGGAGCCAGCTGCACCTAGGAGACACCTTT  
 GTTCTTCAAGCCTGTGGGGGAAGTTCGGGTGCTTATTTTATCTTTCTTGAAGAAAAAATGATAAAAAAT  
 CTCAAAGCTGATTTTCTGTTATAGAAAACTAATAAAGCAATATCCCTATCCCTGCAAAAA

## **FIGURE 108**

MEGEEAEQPAWFHQWPRPGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHLSPEENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVD CGGIDLREFPGDLP  
EHTNHL SLQNNQLEKIYPEELSRLHRL ETLNLQNNRLTSRGLPEKA FEHLTNLNYLYLANNK  
LTLAPRFLPNALISVDFAANYLT KIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMPNGSSNV  
EVLILSSNFLRHVPKHLPPALYK LHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN  
ETFWKLSSELYLDLSSNNLSRV PAGLPRSLVLLHLEKNAIRSDANVLTPIRSLEYLLLSHN  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMILHNQITGIGREDFATTYF  
LEELNLSYNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNE LAALA  
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANAFDSTPNLKGIFLRFNKLA VGSVVDSAFRRLLKHLQVLDIEGNLEFGDISK  
RGRLGKEKEEEEEEEEEEEETR

### **Signal sequence:**

amino acids 1-48

### **N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

### **N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

### **Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557



## **FIGURE 110**

MDFLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCP  
RCKHGEICGPNKCKCHPGYAGKTCNQDLNECGLKPRCKHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCQYGCDDVVKQIRQCQPSGLHLAPDGRTCVDVDECATGRASCPRFRQC  
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDECSLQYQCSSFARCYNVRGSYKCKCKEGYQG  
DGLTCVYIPKVMIEPSGPIHVPKNGTILKGDITGNNNWI PDVGSTWWPPKTPYI PPI ITNRP  
TSKPTTRPTPKPTPIPTPPPPPLPTELRTPLPPTTPTTGLTTIAPAASTPPGGITVDN  
RVQTDPOKPRGDVFSVLVHSCNFDHGLCGWIREKNDLHWEPIRDPAAGQYLTVSAAKAPGG  
KAARLVLPGLRLMHSDDLCLSFHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGGHGWRTQI  
TLRGADIKSESQR

### **Signal sequence:**

amino acids 1-17

### **N-glycosylation site.**

amino acids 273-277

### **Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

### **Tyrosine kinase phosphorylation site.**

amino acids 199-206

### **N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

### **Cell attachment sequence.**

amino acids 382-385

### **EGF-like domain cysteine pattern signature.**

amino acids 75-87

## FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTGTGCCCTTTAGATTGTGA  
AATGTGGCTCAAGGCTTTCACAACCTTTCTTTCTTTGCAACAGGTGCTTGTCTGGGGCTGA  
AGGTGACAGTGGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTCTACCTTACCCGTC  
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA  
CACAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCTGACTTGGAAATACC  
AACACAAGTTTCAACATGATGCCACCCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCCT  
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAGGGAATGGAACCTATCTGCCAGTCA  
GAAGATACAAGTCACGGTTGATGATCCTGTGCACAAAGCCAGTGGTGCAGATTATCCTCCTCT  
CTGGGGCTGTGGAGTATGTGGGGAACATGACCTTGACATGCCATGTGGAAGGGGGCACTCGG  
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC  
TCCCCAAAACAATACCTTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT  
GCCTGTGAGGAACCTGTGAGTGAATGGAAGTGATATCATTATGCCCATCATATATTAT  
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGT  
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGTCTGATTCTCATCCCCCAACACCTACT  
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAAGCATGGGCCTCGCTTAGAAGTT  
GCATCTGAGAAAGTAGCCCAAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC  
CGGCAGGCAAGATGAAACTCATTTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG  
CACAGAAAGGAAAAATCATTGTCACTTTAGCAAGTATAACTGGAATATCATTATTTTGATT  
ATATCCATGTGTCTTCTCTTCCATGGAAAAAATATCAACCCCTACAAGGTTATAAAAACAGAA  
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATG  
CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTTCCAGG  
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGCAAGATTTGCACAGTACAGT  
GTATGAAGTTATTACGACATCCTTCCCAGCAGCAAGACCATCCAGAGTGAACCTTTCATGG  
GCTAAACAGTACATTGAGTGAATTTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAAAAGT  
ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATTCTTTTACA  
TGCAGAAATAGAGGCATTTATGCAAATTGAACTGCAGGTTTTCAGCATATACACAATGTCTT  
GTGCAACAGAAAAACATGTTGGGGAATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGG  
GGAGAACGAAAGTGACAGGGGTTTCTCATAGTTTGTATGAAATATCTCTACAAACCTCA  
ATTAGTTCTACTCTACACTTTCACTATCATCAACACTGAGACTATCCTGTCTCACTACAAA  
TGTGGAAACTTTACATTGTTTCGATTTTTCAGCAGACTTGTGTTTATTAATTTTTTATTAGTG  
TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTATTGTTACAA  
CAAAGTAATAAGGATGGTTGTCAAAAAACAAAATATGCTTCTCTTTTTCATTCACC  
AGTAGTATTTTTGAGAAGACTTGTGAACACTTAAGGAATGACTATTAAAGTCTTATTTTTTA  
TTTTTTTCAAGGAAAGATGGATTCAAATAAATTATCTGTTTTGCTTTTAAAGAAAAA

## **FIGURE 112**

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVRGQALYLPVHYGFTPASDIQIIWLFERPH  
TMPKYLLGSVNKSVVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTLSASQ  
KIQVTVDDPVTQKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS  
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPGYGLQVNSDKGLKVGEVFTV  
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTM DYVCCAYNNIT  
GRQDETHFTVIIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTV  
YEVIQHIIPAQQQDHPE

### **Signal sequence:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 341-359

### **N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

### **Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

### **Tyrosine kinase phosphorylation site.**

amino acids 272-280

### **N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18



## FIGURE 113

GCAAGCGGCGAAATGCGGCCCTCCGGGAGTCTTGCACTTCCCCTGGCAGTCTGGTGTCTGT  
GCTTTGGGGTCTCCTCGGACGCACGGGCGGCGAGCAACGTTTCGCGTCATACGGACGAGA  
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTATGCCCGCTGGTGCCTGTCT  
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTGTGTAATGGGGAGAAGATCTTGAGGTTAA  
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTC  
TTCCCTACTATTTATCATTGTAAAGATGGTGAATTTAGGCCCTATCAGGGTCCAAGGACTAAG  
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGAAGAGTATTGAGCCCGTTTCATCATG  
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGA  
TCAGGACGTGCCATAACTACTTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT  
GTTTTTGTCTTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGC  
AGATTGCCCTTTGTCTTCAAAAAGGCGCAGACCACAGCCATACCCTATCCCTTCAAAAAAT  
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGGCGGATGAAGAA  
GATGTTTCAGAAGAGAAGCTGAAAGTAAAGAAGGAACAACAAAGACTTTCCACAGAATGC  
CATAAGACAACGCTCTCTGGGTCATCATTTGGCCACAGATAAATCCTAGTTAAATTTTATAG  
TTATCTTAATATTATGATTTTGATAAAAACAGAAGATTGATCATTTTGTGTTGGTTGAAGTG  
AACTGTGACTTTTTTGAATATTGCAGGGTTTCAGCTAGATTGTCATTAAATTTGAAGAGTCTA  
CATTCAGAACATAAAAGCACTAGGTATACAAGTTTGAATATGATTTAAGCACAGTATGATG  
GTTTAAATAGTTCTCTAATTTTGAAAAAATCGTGCCAAGCAATAAGATTTATGTATATTTGT  
TTAATAATAACCTATTTCAAGCTGAGTTTGAATAATTTACATTTCCCAAGTATTGCATTAT  
TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTTCTCATTTTGATATAATTTTCTCTG  
TTTCACGTGTGAAAAAAGAGATATTTCCCATAAATGGGAAGTTTGGCCATTGTCTCAAG  
AAATGTGTATTTAGTGACAATTTTCGTGGTCTTTTAGAGGTATATTCCAAAATTTCCCTGT  
ATTTTTAGGTTATGCAACTAATAAAAACTACCTTACATTAATTAATTACAGTTTTCTACACA  
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTTTAAGTTCATGGTATTTCTCTGATTC  
CAACAAAGTTTGATTTTTCTCTGTATTTTTCTTACTTACTATGGGTTACATTTTTATTTTTT  
CAAATTTGGATGATAATTTCTTGAAAAATTTTTATGTTTGTAGTAAACAGTATTTTTTTGTT  
GTTTCAAACCTGAAGTTTACTGAGAGATCCATCAAATGAACAATCTGTTGTAATTTAAAAAT  
TTGGCCACTTTTTTCAGATTTTACATCATTTCTGTCTGAACCTCAACTTGAAATGTTTTTTT  
TTTCTTTTTGGATGTGAAGGTGAACATTTCTGATTTTGTCTGATGTGAAAAAGCCTTGGTA  
TTTTACATTTTGAAAATTCAAAGAAGCTTAATATAAAAGTTTGCAATCTACTCAGGAAAAAG  
CATCTTCTGTATATGCTTAAATGTATTTTGTCTCATATACAGAAAGTTCTTAATTTGAT  
TTTACAGTCTGTAATGCTGTGATGTTTAAATAATAACATTTTTATATTTTTTAAAGACAA  
ACTTCATATTTCTGTGTTCTTTCTGACTGGTAATATTGTGTGGGATTTACAGGTA  
GTCAGTAGGATGGAACATTTTAGTGATTTTACTCTTAAAGAGCTAGATAACATAGATTTT  
CACCTTAAAAAGAGGGGAAAAATCATAAATACAATGAATCACTGACCATTACGTAGTAGG  
AATTTCTGTATATGTCCTTCTTCTAGGCTCTGTTGCTGTGTGAATCCATTAGATTTACAG  
TATCGTAATATACAAGTTTTCTTTAAGCCCTCTCTTTAGAATTTAAATATTGTACCATT  
AAAGATTTGGATGTGTAACTGTGTGATGCTTTAGAAAAATATCCCTAAGCACAAATAAACCT  
TTCTAACCACTTCATTAAGCTGAAAAA  
AAAAAAAAAAAAA

## **FIGURE 114**

MAPSGSLAVPLAVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL  
QPEWESFAEWGEDLEVNI AKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI  
NFISDKWKSI EPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL  
ATLFGSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKLLSESAQPLKKVEEEQEAEDEEDVSE  
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

### **Signal sequence:**

amino acids 1-26

### **Transmembrane domain:**

amino acids 182-201

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

### **Tyrosine kinase phosphorylation site.**

amino acids 107-115

### **N-myristoylation site.**

amino acids 20-26, 192-198

### **Amidation site.**

amino acids 25-29

## FIGURE 115

GCGAGTGTCAGCTGCGGAGACCCGTGATAATTCGTTAACTAATTCACAAACGGGACCCCTT  
CTGTGTGCCAGAAACCCCAAGCAGTTGCTAACCCAGTGGGACAGCGCGGATTGGGAAGAGCGGG  
AAGGTCCTGGCCCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC  
ATTGCTGATGGCCTGGTTTGGTGTCTGAGCTGTGTGCAGGCCGAATCTTTCACCTCTATTG  
GGCAGACTGACCTGATTTATGTCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC  
CTTTGGAGGAAGCCAAAGCTTCCAAAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTTGAC  
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG  
TGAAGCGGCTAAACACAGACTGGCCTGCCTGGAGGACCTTGCTCTGCAGGACTCAGCTGCA  
GGTTTTATCGCCAACTCTCTGTGCAGCGGCAGTTCTCCCCACTGATGAGGACGAGATAGG  
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCAGGCACAAATTTCCA  
GAGGGGAACCTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG  
GGCCGCTCGGCCTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT  
AAAGCAGCTTGATGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA  
GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCGCCTGCTC  
TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA  
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAAGGCA  
TCTATGAGAGGCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGTGG  
GAGGTGTCAAACCTGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAA  
CAGGGCCCCACAGCTGCTCATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACA  
TCGTCAGGTACTACGATGTCATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA  
CCTAAACTTGCACGAGCCACCGTTCTGTGATCCCAAGACAGGAGTCTCTACTGTGCGCAGCTA  
CCGGGTTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCTGTGTGGCCCGAGTAAATC  
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCGAAATGTGTACAGGTTGCAAAAT  
TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGCGGACCTTTTGACAGCGG  
CCTCAAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGTATGTAGAAGCTG  
GTGGTGCCACCGTCTTCCCTGATCTGGGGCTGCAATTTGGCCTAAGAAAGGTCACAGCTGTG  
TTCTGGTACAACCTCTTGGGAGCGGGGAAGGTGACTACCGAACAAGACATGCTGCTGCCCTGCC  
TGTGCTTGTGGGTGCAAGTGGGTCTCCAATAAGTGTTTCCATGAACGAGGACAGGAGTCTT  
TGAGACCTTGTGGATCAACAGAAGTTGACTGACATCCTTTTCTGTCTCTCCCTTCCCTGGTC  
CTTCAGCCCATGTCAACGTGACAGACACCTTTGTATGTTCCTTTGTATGTTCCATCAGGCT  
GATTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACATACTAGGGGCACTCCTGT  
GTGACTGAAGTCCAGCCCTTCCATTGAGCCTGTGCCATCCTTGCCGCCAAGGCTAGGATCA  
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTTGTACCTCAGGTGTT  
TTAGGTGTGAGATGTTTCAGTGAACCAAAGTCTGATACCTTGTTTACATGTTTGTTTTTAT  
GGCATTTCATCTATTGTGGCTTTACCAAAAAATAAAATGTCCCTACAGAAAAA

## **FIGURE 116**

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKISWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDVLVQDSAAGFIANLSVQRQFFP  
TDEDEIGAALMRLQDITYRLDPGTISRGEIPGTTYQAMLSVDDCFGMGRSAYNEGYYHTV  
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLLSLDPSHERAGGNLR  
YFEQLLEEREKTLTNQTEAELATPEGIYERPDVYLPERDVYESLCRGEQVGLTPRRQKRLF  
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYVDVMSDEEIERIKEIAKPKLARATVRDPKTF  
VLTVASYRVSKSSWLEEDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS  
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEQDYR  
TRHAACPVLVGCKWVSNKWFERHGEFLRPCGSTEVD

### **Signal sequence:**

amino acids 1-17

### **N-glycosylation site.**

amino acids 115-119, 264-268

### **Glycosaminoglycan attachment site.**

amino acids 490-494

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

### **Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

### **Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

### **N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

### **Leucine zipper pattern.**

amino acids 213-235

## FIGURE 117

GCAGTATTGAGTTTACTTCCTCTCTTTTTAGTGGGAAGACAGACCATAATCCCAGCTGTGAGTGAAATGATTGT  
 TTCATTATTACCGTTTGGCTGGGGTGTAGTTCGACACCTTTCACAGTTGAAGAGCAGGCAGAGGAGTTGTGA  
 AGACAGGACAACTCTTGGGGATGCTGGTCTGGAAGCCAGCGGGCTTGTCTGTCTTTGGCCTCAITGACCC  
 CAGGTTCTCTGGTTAAAACTGAAAGCCTACTACTGGCCTGGTGCCCATCAATCCATTGATCCTTGAGGCTGTGCC  
 CCTGGGGACAGCACTTGGCAGGGCTTACCACCTATGCGACTGAGCTCCCTGTGGCTCTGCTGGCGCCACGCTTC  
 CCCCTCATCTTAGGCTGTCTCTGGGGTGCAGCCTGAGCCTCCTGTGGGTTTCTCGGATCCAGGGGAGGGAGAG  
 ATCCCTGTGTGTGAGGCTGTAGGGGAGCAGGAGGGCCACAGAAATCCAGATTTCGAGAGCTCGGCTAGACCAAAGTG  
 ATGAAGACTTCAAAACCCCGGATTGTCCCTTACTACAGGGACCCCAACAGCCCTACAAGAAGGTGTCTGAGGACTC  
 GGTACATCCAGACAGAGCTGGGCTCCCTGAGCGGTTGCTGGTGGCTGTCTTGACCTCCCGAGCTACACTGTCCA  
 CTTTGGCCGTGGCTGTGAACCGTACGGTGGCCCATCACTTCCCTCGGTACTTACTTCACTGGGCAGCGGGGG  
 CCGGGCTCCAGCAGGAGTGCAGGTGGTGTCTCATGGGGATGAGCGGCCCGCTGGCTCATGTCCAGAGACCCGTGC  
 GCCACCTTCAACACACTTGGGGCCGACTACGACTGGTCTTTCATCATGTCAGGATGACATATGTGCAGGCC  
 CCGCCTGGCAGCCCTTGTCTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGCAGAGGAGTTCAATG  
 GCGCAGGCGCAGGCCCCGTATGTCTATGGGGCTTTGGCTACCTGTGTGTCAGCGAGTCTCTGTCTTGTCTGTCTG  
 GGCACATCTGGATGCTCCGAGGAGACATTCTCAGTGCCCTCTGACGAGTGGCTTGGACGCTGCCCTCATTG  
 ACTCTCTGGGCTCGCTGTGTCTCACAGCACCGGGGCGAGCATATCGCTCATTTGAACTGGCCAAAAATAGGG  
 ACCCTGAGAAGGAAGGAGCTCGGCTTCTCAGTGGCTTGGCCGTGACCTCTTGTCTCCGAAGTACCTCATGT  
 ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCGGGCTTACAGTGAATAGAACACTGTCAGGCTCAGA  
 TCCGGAACCTGACGCTGTGACCCCCGAAGGGGAGGCGAGGCTGAGCTGGCCGTTGGGCTCCCTGCTCCTTTCA  
 CACCACTCTCGCTTTGAGGTGTGGGCTGGGACTACTTCAACAGAGCAGCACACTTCTCTCTGTGTCAGATGGG  
 CTCCCAAGTGCCCACTACAGGGGGCTAGCAGGGCGGACGTGGGTGATGCGTTGGAGACTGCTCCTTGAGCAGCTCA  
 ATCGCGCTATCAGCCCGCTCGGCTTCCAGAAGCAGCGACTGCTCAACGGCTCTCGGCTTCCAGCCAGCAGC  
 GGGCATGGAGTACACCTTGAACCTGTCTTGGAAATGTGTGACACAGCGTGGGCACCGCGGGGCCCTGGCTCGCA  
 GGGTCAGCTTCTGCGGCCACTGAGCGGGTGGAAATCCTACTATGCCCTATGTCTCATGAGGCCACCGAGTGC  
 AGCTGTGTCTGCCACTCTGTGTGGCTGAAGCTGTGTCAGCCCCGGCTTCTCTGAGCGGCTTTGTCAGCCAATGTCC  
 TGGAGCCACGAGAACATGCATTGTCTCACCTTGTGTGGTCTACGGGCCACGAGAAGGTGGCCGTGGAGCTCCAG  
 ACCATTTCTTGGGGTGAAGGCTGCAGCAGCGGAGTTAGAGCGACGGTACCCTGGGACGAGGCTGGCCTGGCTCG  
 CTGTGCGAGCAGAGGCCCTTCCAGGTGCGACTCATGGAAGTGGTCTCGAAGAAGCACCTGTGGACACTCTCT  
 TCTTCTTACACCGCTGTGGAAGGGCTGGGCCGAAGTCTCAACCGCTGTGCGATGAATGCCATCTCTGGCT  
 GGCAGGCTTCTTTCAGTTCATTTCCAGGAGTTCAATCTGCTCCTGTACACAGAGATCACCCCGAGGGCCCC  
 CGGGGCTGGCCCTGACCCGCCCTCCCTCTTGGTGTGACCCCTCCCGGGGGGCTCTTATAGGGGGAGATTG  
 ACCGGCAGGCTTCTGCGGAGGGCTGCTTCTAACACGCTGACTACCTGGCGGCCGAGCCCGGCTGGCAGGTGAAC  
 TGGCAGGCCAGGAAGAGGAGGAGCCCTGGAGGGCTGGAGGTGATGATGTTTCTCTCGGTTCTCAGGGCTCC  
 ACCTCTTTGGGGCGTAGAGCCAGGGCTGGTGCAGAAAGTTCTCCCTGCGAGACTGCAGCCCAAGGCTCAGTGAAG  
 AACTCTACACCGCTGCCCTCAGCAACTGGAGGGGCTAGGGGGCCGTGCCAGCTGGCTATGGCTCTCTTTG  
 AGCAGGAGCAGCCAAATAGCACTTAGCCGCTGGGGCCCTAACCTCATTACCTTCTCTTGTCTGCTCAGCC  
 CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGGAATGTGTGCTATTTTTAAATATGAAGAAATGTTATTAA  
 ACATGTCTTCTGCC

## FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSSRRLD  
QSDDEFKPRIVPYRDPNPKPYKKVLTRYIQTGLGSRERLLVAVLTSRATLSTLAVAVNRTV  
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSSETLRHLHTHFGADYDWWFFIMQDDTY  
VQAPRLAALAGHLSTINQDLYLGRABEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG  
DILSARPDWEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFVHPVSE  
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEV  
LGWDYFTEQHTFSCADGAPKCPQLQGASRADVGDALETALEQLNRRYQPRLRFQKQRLLLNGYR  
RFDPARMEYITLDLLECEVTQQRGHRRALARRVSLRLPLSRVEILPMPYVTEATRVQLVLPLL  
VAEAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAAELERRYPG  
TRLAHLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTVTWTRPGPEVLNRCRMNAISGWQAFPP  
VHFQEFNPALSPQRSPPGPPGAGDPDPPSPPGADPSRGAPICGRFDRQASAEGCFYNADYLAA  
RARLAGELAGQEEEEALEGLEVMDFLRFSGLHLFRAVEPLGVKQFSLRDCSPRLSEELYHR  
CRLSNLEGLGGRAQLAMALFEQEQANST

### Signal sequence:

amino acids 1-15

### Transmembrane domain:

amino acids 489-507

### N-glycosylation site.

amino acids 121-125, 342-346

### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

### Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

### Tyrosine kinase phosphorylation site.

amino acids 736-743

### N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

### Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

### Cell attachment sequence.

amino acids 247-250

## FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGGGCTGCGCTTTCCTGTCCCCAAGCC  
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG  
AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAAATTCA  
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTGAGTATACTGTATTATCCTTGTAAGAAC  
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACTGTGACAAAGCAG  
AGTTCTTCAGTTCTGAAAAATGTTAAAGTGTGTTGAGTCAATTAATATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACCTG  
GTTCTTCCTTGACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAA  
AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT  
GTGGGTATGGAAGGAGGAATGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT  
CAATATCCCAGAAAAGTGTCTTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC  
AGCTAGCAGTTTGCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA  
AAAGATGTATTTAATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCC  
CAACCAGGTAGTAGAAGGCTGTGTTGAGATATGGCTGTTACTTTTAATGGACTGACTCCAA  
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTGGGCATATTTTCAAT  
GATGCATTGTTTTCTTACCTCCAAATGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCG  
TGAATATGATCTTTGTATAGGACGTGTGTTGTCTATTATTGTAGTAGTAACATACATATCAA  
TACAGCTGTATGTTTTCTTTTCTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAG  
TCAGTAGTACATTTTAAATGAGGGTGGTTTTTTCTTTAAACACATGAACATTGTAAATG  
TGTTGGAAGAAGTGTTTTAAAGAATAATAATTTGCAAATAAACTATTAATAAATATTATAT  
GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGCACATATTTTGTGATTTGGTT  
AAAAAATTTTAAAGGTCCTTTAGCGTTCTAAGATATGCAAAATGATATCTCTAGTTGTGAATT  
TGTGATTAAAGTAAACTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCT  
AAGCCTCCCCAAGTTCCAATGGATTGTCCTTCTCAAATGTACAACCTAAGCAACTAAAGAAA  
ATTAAAGTGAAAGTTGAAAAAT

## **FIGURE 120**

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDI LKISEDERME  
LSKSPRVYCIILVKPKDVS LWAAVKETWTKHCDKAEFFSSENVKVPESINMDTNDMWLMMRK  
AYKYAFDKYRDQYNWFFLARPTTFAI IENLKYFL LKKDPSQPFYLGHTIKSGDLEYVGM EGG  
IVLSVESMKRLNSLLNIPEKCPEQGGM IWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL  
PPNGSDND

### **Signal sequence:**

amino acids 1-33

### **N-glycosylation site.**

amino acids 121-125, 342-346

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

### **Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

### **Tyrosine kinase phosphorylation site.**

amino acids 736-743

### **N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

### **Cell attachment sequence.**

amino acids 247-250



[illegible][illegible]

## **FIGURE 122**

MNSSKSSETQCTERGCFSQMFLLWTAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALS LKNC SAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLS DQVVEGQWQVWDGTP LTKSLSFWDVGE PNNIATLED CATMRDSS  
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

### **Signal sequence:**

amino acids 1-42

### **N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

### **N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

## FIGURE 123

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCTCAGCAACCTCGACATGCGGCTGAGGCGGCCAACCCGCGAC  
 TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAATATC  
 TCAAAATCCAGCAATCGAAACCCAGCTGGTACAGGAATTTGAAAGTGTGGAACCTGTCTGCATCATTCGGATTTCGC  
 AGACAAGTGACCCAGGATCGAGTGGAGAAAAATCAAGATGAAACAAACACATATGTGTTTTTGACAAACAAA  
 TCTCAGGAGACTTGGCGGGTGGTCAGAAAAATCTGGGGAGAGACATCCCTCAAGATCTGGAAATGTGACACGGAGAG  
 ACTCAGCCCTTATCGCTGTGAGGTGCTGTCTCGAAATGACCGCAAGGAAATGATGAGATTGTGATCGAGTTAA  
 CTGTGCAAGTGAAGCCAGTGAACCCCTGTCTGTAGAGTGGCGAAGGCTGTACCAAGAGATGGCAACACTGC  
 ACTGCCAGAGAGTGAAGGGCCACCCCGGCGCTCACTACAGCTGGTATCGCAATGATGTACCATGTGCCACGGATT  
 CCAGAGCCCAATCCAGATTTCGCAATTTCTTTCCACTTAACTCTGAAACAGGCACCTTTGGTGTTCACTGCTG  
 TTCACAAGGACGACTCTGGGAGTACTACTGCTATGCTTCCAATGACGAGGCTCAGCCAGGTGTGAGGAGCAGG  
 AGATGGAACTCTATGACTGAACCATTTGGCGGAATTAATGGGGGGTCTGGTTGTCTTGTCTGCTGCTGACCTGC  
 TCACGTGGGCACTCTGCTGTGCATACAGAGCTGGCTACTTCATCAACAAATAACAGGATGGAGAAAGTTACAAGA  
 ACCCAGGGAACAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGGCACTTCAGACACAAGTCATCGTTTG  
 TGATCTGAGACCCCGGCTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAACTCTCTGTCAA  
 GGCAGCGAGAGCTGATGCACCTCGGACAGAGCTAGACACTCATTCAGAAGCTTTTCGTTTGGCCAAAGTTGACCA  
 CTACTCTTCTTACTCTAAACAGCCACATGAATAGAAGAAATTTTCCTCAAGATGGACCCGGTAAATATAACCAAA  
 GGAAGCGAAAACGGGTGCTTCCATGAGTTGGGTTCTTAATCTGTTCTGGCCCTGATCCCGCATGAGTATTAGG  
 GTGATCTTAAAGAGTTTGTCTACGTAACCGCCGTGCTGGGCCCTGTGAAGCCAGCATGTTCCACACTGGTCTGT  
 CAGCAGCCACAGCAGCACCATGTGAGATGGCGAGGTGGCTGACAGCACAGCAGCGCATCCCGCGGGAACCCA  
 GAAAAGGCTTCTTACACAGCAGCTTACTTTCATCGGCCACAGACACCCAGCTTTCTCTTAAAGCTCTGC  
 TGATCGGTGTGCGAGTGCATTTGTGGAGAAGCTTTTGGATCAGCAATTTGTAAACACCAACAAATCAGGAAG  
 GTAAATTTGGTTGTGGAAGAGGCTTTCCTGAGGAACCTGCTGTGTCACACAGGGTGTCCAGGATTTAAAGAAA  
 ACCTTCGCTCTAGGCTAAGTCTGAATGTTACTGAAATATGCTTTTCTATGGGTCTTGTTTATTTTATAAAATTT  
 TACATCTAAATTTTGTCTAAGATGTATTTTGATTATTGAAAGAAATTTCTAATTAACCTGTAATATATTTG  
 CATACAATGTTAAATAACCTATTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTTGTAAAT  
 TGGAAAATCAATAATTAAGATATTTTACCAGGAATCTCTCATGGAAGTTTACTGTGATGTTCCTTTCTTCT  
 CACACAAGTTTATGCTTTTTCACAAGGGAACCTCATCTGTCTACACATCAGACCATAGTTGTCTAGGAAACCTT  
 TAAAAATCCAGTTAAGCAATGTTGAAATCAGTTTGCACTCTCTTCAAAAGAAACCTCTCCAGGTTAGCTTTGAACT  
 GCCTCTTCTGAGATGACTAGGACAGTCTGTACCAGAGGCCACCCAGAGCCCTCAGATGTACATACACAGATG  
 CCACTCAGCTCTGGGGTTGGCCAGGCGCCCGGCTCTAGCTCACTGTTGCCCTCGCTGTGCCAGGAGGCCCT  
 GCCATCTTGGGCCCTGGCAGTGGCTGTGTCCAGTGAGCTTACTCACTGCTGGCCCTGCTTCACTCCAGCACAGC  
 TCTCAGGTGGGCACTGCAGGGAACCTGTTGCTTCCATGTAGCGTCCAGCTTTGGGCTCCTGTAAACAGACCTCT  
 TTTTGGTTATGGATGCTCACAATAAGGGCCCCCAATGCTATTTTCTTTTAAAGTTTGTTTAATTAATTTGTT  
 AAGATTCTAAGGCCAACAGCAATTCGGAATCAAGTCTGCAAGTACAAATCAATTTTAAAAAGAAATGGAT  
 CCCACTGTTCTCTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTCAAAACAAACCATGAT  
 GGAGTGGCGCCGAGCTCAGCCCTTTTAAAGAACCTCAGGTGGAGCAGCCAGGTGAAAGCCCTGGCGGGGAGGAAAG  
 TGAACGCTGAATCAAAGCAGTTTTCTAATTTGACTTTAAATTTTTCATCCGCGGAGACACTGCTCCCAAT  
 TGTGGGGGACATAGCAACATCACTCAGAAGCCTGTGTTCTCAAGAGCAGGTGTTCTCAGCTCATGTGCCCT  
 CGCGTCTGGACTCAGGACTGAAGTGTGTAAAGCAAGGAGCTGTCTGAGAAGGAGCACTCCACTGTGTGCCCTGGA  
 GAATGGCTCTCACTCACTCCTTGTCTTTCAGCTTCCAGTGTCTGGGTTTTTATATCTTTGACAGCTTTTTTTT  
 AATTTGCACTGACAGCTGTGTGACTTTTGTAGTTATGTGAACACCTTTGCCGAGGCCGCTGGCAGAGGCA  
 GGAATGTCTCAGCAGCTGGCTGAGCTTCCCTGGTGTCTGCTGCATGGCATCTGAGATCTTGCATGCAAGTTC  
 CCTCCTGTTCTTCCACTTGTGTAGAGAGGGATGGCTCCCCACCTCAGCGTGGGAGTTACGCTCTCAGCCTCTCT  
 TCTTGTGTGTCACTGATGAGGTAGGCTTATGTGCCCTCTCTTATACCTTAAACCTCTCACTACAGTGCCTA  
 TGGGAACAGGCTCTGAAAAGTAGAGGAAGTGAAGTAGAGTCTGGGAAGTAGTCTGCTTAAGTCTGAGACTAGA  
 CGGAAAAGAACTACTGCTGTTTAAAGATAGAATGTGACTCAAGACTCAGGCGGATGACAGGCTGTGATTCT  
 GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACCCGTAATTTGGCACTTGTTTAAC  
 CTCATTTATAAAGCTTCAAAAAAACCA

CCAGGCTGAGGCGGCCAACCCGCGAC

## **FIGURE 124**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTFVVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQSESGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDNLNIGGIIGG
VLVVLAVLALITLIGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-30

#### **Transmembrane domain:**

amino acids 243-263

#### **N-glycosylation sites.**

amino acids 104-107, 192-195

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

#### **Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

#### **Tyrosine kinase phosphorylation site.**

amino acids 69-77

#### **N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267